

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 17, 2006, 10:49:16 ; Search time 1231 Seconds
(without alignments)
3347.359 Million cell updates/sec

Title: US-10-733-816-2
Perfect score: 2081
Sequence: 1 MEYMPMEGGMGRPTTSP.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/abs/ABSSWEB.spool/US10733816/runat.15092006.085442.15433/app_query.fasta.1
-DB=N Geneseq -QFWT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10733816 @CGN 1.1 2019 @runat.15092006.085442.15433 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 8.:

1:	Geneseqn1980s.*
2:	Geneseqn1990s.*
3:	Geneseqn2000s.*
4:	Geneseqn2001as.*
5:	Geneseqn2001bs.*
6:	Geneseqn2002as.*
7:	Geneseqn2002bs.*
8:	Geneseqn2003as.*
9:	Geneseqn2003bs.*
10:	Geneseqn2003cs.*
11:	Geneseqn2003ds.*
12:	Geneseqn2004as.*
13:	Geneseqn2004bs.*
14:	Geneseqn2005s.*
15:	Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2024	97.3	1260	13 ADT92556	Adt92556 Human gly
2	2024	97.3	1389	4 AAD1491	Aad1491 Human gly
3	2024	97.3	1389	10 ACA56816	Aca56816 Human sig

4	2024	97.3	1389	10 ADK11466	Adk11466 Human gly
5	2024	97.3	1389	12 ADI56612	Adi56612 Human pol
6	2024	97.3	1389	13 ADRA0190	Adra0190 Human gly
7	2015	96.8	1525	10 ADB53390	Adb53390 Primary r
8	2015	96.8	1525	14 AEA62866	Aea62866 Rat glyco
9	2015	96.8	1972	2 AAQ67459	Aaq67459 Codes tau
10	2015	96.8	1972	10 ADB68695	Adb68695 Rat tau p
11	2013	96.7	1600	14 AEE06397	Aee06397 Glycogen
12	2013	96.7	1815	5 ABV30267	Abv30267 Human pro
13	2012	96.7	1474	14 AEA62868	Aea62868 Rat glyco
14	2010	96.6	1503	12 ADI28892	Adi28892 Mouse gly
15	2010	96.6	2088	2 AAQ67458	Aaq67458 Codes tau
16	1996.5	95.9	1579	15 AEE92755	Aef92755 Human GSK
17	1996.5	95.9	1639	9 ACC78383	Acc78383 Human gly
18	1996.5	95.9	1639	12 ADO49106	Ado49106 Human ded
19	1996.5	95.9	1639	13 ADS92934	Ads92934 Glycogen
20	1996.5	95.9	1639	13 ADR66574	Adr66574 Human pro
21	1996.5	95.9	1639	13 ADR66232	Adr66232 Human pro
22	1996.5	95.9	1639	13 ADU20924	Adu20924 Human gly
23	1996.5	95.9	1639	13 ADU05922	Adu05922 Novel bro
24	1996.5	95.9	1639	14 ADZ48946	Adz48946 Insulin s
25	1996.5	95.9	1639	14 AEB25736	Aeb25736 DNA encod
26	1996.5	95.9	1639	14 AEC34200	Aec34200 Human GSK
27	1996.5	95.9	1639	14 AEC81934	Aec81934 DNA encod
28	1996.5	95.9	1639	14 AER06395	Aer06395 Glycogen
29	1986	95.4	1230	10 ADR66952	Adr66952 Gene #42
30	1919	92.2	1501	14 AEE06401	Aee06401 Glycogen
31	1902.5	91.4	1540	14 AER06399	Aer06399 Glycogen
32	1634.5	78.5	1698	10 ADC99112	Adc99112 Human KPP
33	1609	77.3	1952	12 ADI61656	Adi61656 Human CDN
34	1609	77.3	1952	14 AEA43821	Aea43821 Human CDN
35	1609	77.3	2154	4 AAD14750	Aad14750 Human gly
36	1609	77.3	2169	9 ABK83893	Abk83893 Human CDN
37	1609	77.3	2169	9 ACC78382	Acc78382 Human gly
38	1609	77.3	2169	13 ADU18030	Adu18030 Human can
39	1609	77.3	2169	14 ADZ48945	Adz48945 Insulin s
40	1609	77.3	2169	14 AEC10094	Aec10094 Human gly
41	1609	77.3	2170	9 ACC78381	Acc78381 Human gly
42	1609	77.3	2189	14 AEC81933	Aec81933 DNA encod
43	1609	77.3	2374	12 ADQ21777	Adq21777 Human sof
44	1607	77.2	2155	10 ADB58321	Adb58321 Toxicity-
45	1607	77.2	2155	13 ADV41141	Adv41141 Rat cardi

ALIGNMENTS

RESULT 1
ADT92556
ID ADT92556 standard; DNA; 1260 BP.
XX
AC ADT92556;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human glycogen synthase kinase-3-related coding sequence - SEQ ID 2.

XX
KW neurogenerative drug; glycogen synthase kinase-3; GSK-3;
KW neurological disease; Parkinson's disease; Alzheimer's disease;
KW Down's syndrome; cerebrovascular accident; stroke; spinal injury;
KW Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis;
KW epilepsy; anxiety disorder; schizophrenia; depression;
KW manic-depressive psychosis; gene; ds.
XX
OS Homo sapiens.

PH	Key	Location/Qualifiers
FT	CDS	1..1260
FT		/*tag= a
FT		/partial
FT		/product= "Human glycogen synthase kinase-3-related
FT		protein"
FT		/note= "No stop codon is given"
XX		

PN WO2004091663-A1.
 XX 28-OCT-2004.
 XX 16-APR-2004; 2004WO-JP005503.
 XX 18-APR-2003; 2003JP-00114579.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Morishita T, Sakurada K, Suzuki K, Ikeda S;
 XX WPI, 2004-784511/77.
 XX P-PSDB; ADT92555.
 XX Neurodegenerative drug for treating neurological disease e.g. Parkinson's
 PT disease, Alzheimer's disease and Down's syndrome, contains substance
 PT which inhibits activity of glycogen synthase kinase-3 as active
 PT ingredient.
 XX Disclosure; SEQ ID NO 2; 115pp; Japanese.
 XX The invention comprises a neurodegenerative drug that inhibits the
 CC activity of glycogen synthase kinase-3 (GSK-3). The neurodegenerative
 CC drug of the invention is useful for treating neurological disease, such
 CC as: Parkinson's disease, Alzheimer's disease, Down's syndrome,
 CC cerebrovascular accident, stroke, spinal injury, Huntington's chorea,
 CC multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, anxiety
 CC disorder, schizophrenia, depression and manic-depressive psychosis. The
 CC present human DNA sequence is used in the exemplification of the
 CC invention.
 XX SQ Sequence 1260 BP; 358 A; 300 C; 290 G; 312 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.34e-212 Length: 1260
 Score: 2024.00 Matches: 384
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 97.3% Indels: 0
 DB: 13 Gaps: 0

US-10-733-816-2 (1-394) x ADT92556 (1-1260)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
 Db 1 ATGTTCAGGGGGCCAGAACCCCTCTCTTTGGGAGAGCTGCAAGCCGGTGCAGCAGCT 60
 Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
 Db 61 TCAGCTTTTGGCAGCATGAAGATTAGCAGAGACAAAGCCGCGCAGCAAGGTGCACACAGTG 120
 Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThrAspThrLys 70
 Db 121 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTCAGCTATACAGACACTAAA 180
 Qy 71 ValIleGlyAenGlySerPheGlyValValThrGlnAlaLysLeuCysAspSerGlyGlu 90
 Db 181 GTGATTGGAAATGGATCATTTGGTGGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 240
 Qy 91 LeuValAlaIleLysValLeuGlnAspLysArgPheLysAenArgGluLeuGlnIle 110
 Db 241 CTGGTCGCCATCAAGAAGATTATTCAGGACAAAGAGATTTAAGAAATCAGAGACTCCAGATC 300
 Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
 Db 301 ATGAGAAAGCTAGATCACTGTAAACATAGTCGATGGTATTCTTCTTCTCTCCAGGTGT 360
 Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
 Db 361 GAGAAGAAGATGAGGTCTATCTTAATCTGGTGTGAGCATATGTTCCGGAACAGTATAC 420
 Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170

Db 421 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480
 Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 Db 481 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCATTCCTTTTGGAAATCTCCCATCGG 540
 Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
 Db 541 GATATTAAACCCGAGAACCTCTTTTGGATCCTGTGATCTGTATATAAAACTCTGTGAC 600
 Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 Db 601 TTTGGAGTGCAGAACGAGCTGTCCGAGGAGAACCAATGTTTCGTATATCTGTCTCGG 660
 Qy 231 TyrTyrArgAlaProGluLeuPheGlyAlaThrAspTyrThrSerSerIleAspVal 250
 Db 661 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 720
 Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 Db 721 TGGTCTGCTGGCTGTGTGGCTGAGCTGTACTAGGACAAACAATATTTCCAGGGGAT 780
 Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
 Db 781 AGTGGTGTGATCAGTGTGTAGAAATATCAAGTCTCTGGAACTCCACACAGGGAGCAA 840
 Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
 Db 841 ATCAGAGAAATGAACCAACTACACAGAAATTTAAATTTCCCTCAAATTAAGGCACATCCT 900
 Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
 Db 901 TGGACTAAGGTCTTCCGACCCCGAATCCACCGAGGCAATTGCACGTGTGTAGCCGCTG 960
 Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
 Db 961 CTGGAGTATACACCAACTGCCGACCTAACCACTGGAGCTTGTGCACATTCATTTT 1020
 Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
 Db 1021 GATGAATTCAGGAGCCCAATGTCAAAATCCAAATCCAAATGGGCGAGACACACCTGCACCTTC 1080
 Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
 Db 1081 AACTTCACCACTCAAGAAGTGTCAAGTAAATCCACCTCTGGCTACCATCTTATTCCTCT 1140
 Qy 391 HisAlaArgIle 394
 Db 1141 CATGCTCGGATT 1152

RESULT 2
 AAD11491
 ID AAD11491 standard; DNA; 1389 BP.
 XX
 AC AAD11491;
 XX 24-SBP-2001 (first entry)
 DT
 XX Human glycogen synthase kinase 3-beta DNA #1.
 DE
 XX Antisense; glycogen synthase kinase 3-beta; GSK3B; diabetes; infection;
 KW insulin regulation disorder; neurological disorder; Alzheimer's disease;
 KW bipolar illness; inflammation; tumour; tau protein kinase 1; tpk-1;
 XX human; ds.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS /.*tag= a
 FT /product= "Glycogen synthase kinase 3-beta #1"

PN WO200152862-A1.
 XX 26-JUL-2001.
 XX 12-JAN-2001; 2001WO-US001085.
 XX 19-JAN-2000; 2000US-00489765.
 XX (ISIS-) ISIS PHARM INC.
 XX Butler MM, McKay R, Monia BP, Wyatt JR;
 XX WPI; 2001-457510/49.
 DR P-PSDB; AAE05998.
 XX
 PT Novel antisense compounds, particularly antisense oligonucleotides for
 PT inhibiting expression of glycogen synthase kinase 3 beta in cells and for
 PT diagnosing, treating neurological and insulin regulation disorders.
 XX
 PS Example 13; Page 88-90; 106pp; English.
 XX
 CC The invention relates to antisense compounds targetted to nucleic acid
 CC encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau
 CC protein kinase I (TPK-I)). The antisense compound is useful for
 CC inhibiting the expression of glycogen synthase kinase 3-beta enzyme in
 CC cells or tissues and for treating diseases or conditions associated with
 CC the enzyme such as insulin regulation disorder, in particular diabetes
 CC and neurological disorder, e.g. Alzheimer's disease and bipolar illness.
 CC The antisense compound is also useful for diagnosing diseases associated
 CC with the expression of glycogen synthase kinase 3-beta and for
 CC prophylaxis e.g. to prevent or delay infection, inflammation or tumour
 CC formation and as a research reagent. The present sequence is human
 CC glycogen synthase kinase 3-beta DNA
 XX
 SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 1,55e-212 Length: 1389
 Score: 2024.00 Matches: 384
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 97.3% Indels: 0
 DB: 4 Gaps: 0

US-10-733-816-2 (1-394) x AAD11491 (1-1389)

QY 11 MetSerGlyValArgProGlyThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
 DB 40 ATGTCAGGGCGGCCAGAACCACTCTTTTGGGAGAGCTGCAAGCGGTGACAGCCT 99
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
 DB 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGAGCAGCGCAGCAAGGTGACACAGTG 159
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThrAspThrLys 70
 DB 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTCAAGTATACAGACACTAA 219
 QY 71 ValIleGlyAsnGlySerPheGlyValValValThrAlaLysLeuCysAspSerGlyGlu 90
 DB 220 GTGATGGAAATGGATCATTTGGTGGTATATCAAGCCAAACTTTGTGATTGAGAGAA 279
 QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
 DB 280 CTGGTGGCCATCAAGAAGATTATTCAGGACAGAGATTTAAGATCGAGAGCTCCAGATC 339
 QY 111 MetArgLysLeuAspHisCysAenIleValArgLeuArgThrPhePheThrSerSergly 130
 DB 340 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGGTTATTCTTCTACTCCAGTGT 399
 QY 131 GluLysLysAspGluValThrLeuAsnLeuValLeuAspThrValProGluThrValThr 150
 DB 400 GAGAAAGAAAGATGAGGTCTATCTTAATCTGGTGTGGACTATGTTCGGAAACAGTATAC 459

QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
 DB 460 AGAGTTTGCAGACACTATATGTCGAGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 DB 520 TATATGTATCAGCTGTTCGAAAGTTTAGCTATATCATCTCTTTGGAAATCTGCCATCGG 579
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
 DB 580 GATATTAAACCCGACAGAACCTCTTTGTTGGATCTCTGATCTGTATTAAACCTCTGTGAC 639
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 DB 640 TTTGGAAGTGCAGAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 699
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
 DB 700 TACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 DB 760 TGGTCTGCTGGCTGTGTGTTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGAT 819
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
 DB 820 AGTGTGTGTGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGGAGCAA 879
 QY 291 IleArgGluMetAsnProGlyThrGluPheLysPheProGlnIleLysAlaHisPro 310
 DB 880 ATCAGAGAATGAACCAACTACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
 QY 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu 330
 DB 940 TGGACTAAGSTCTTCCGACCCCGAACTCCACCGAGGCAATTGCACTGTGTAGCCGCTG 999
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
 DB 1000 CTGGAGTATACACCAACTGCCGACCTAACACCACTGGAAGCTTGTGCACATTCATTTTT 1059
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyValArgAspThrProAlaLeuPhe 370
 DB 1060 GATGAATTCGGGACCCCAATGTCAAACATCCAAATGGGGGACACACCTGCACCTCTC 1119
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProLeuAlaThrIleLeuIleProPro 390
 DB 1120 AACTTCACCACTCAAGAACTGTCAAGTAAATCCACCTCTGGCTACCATCTTATTCCTCT 1179
 QY 391 HisAlaArgIle 394
 DB 1180 CATGCTCGGATT 1191

RESULT 3
 ACA56816
 ID ACA56816 standard; cDNA; 1389 BP.
 XX
 AC ACA56816;
 XX
 DT 06-JUN-2003 (first entry)
 XX
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1414.
 XX
 KW Human; probe; ss; array element; Parkinson's disease;
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.
 XX
 PN US6500938-B1.
 XX
 PD 31-DEC-2002.
 XX

```

PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
XX
PS Claim 1; SEQ ID NO 1414; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500939B1
XX
SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,55e-212 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 10 Gaps: 0

US-10-733-816-2 (1-394) x ACA56816 (1-1389)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTGAGGGGGCCAGAACACCTCTCTTTGGGAGAGCTGCAAGCGGTGCGAGACGCT 99
QY 31 SerAlaPheGlySerMetLysValSerArcAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAAAGGCGGACGACAGGTCGACAAAGTG 159
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTCAGCTATACAGACACTAA 219
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCCAGAGAA 279
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGTGTCCTCCATCAAGAAGATTTCAGACAGCAAGAGATTTAAGATTCAGAGCTCCAGATC 339
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130

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RESULT 4

ADK11466

ID ADK11466 standard; DNA; 1389 BP.

XX AC

XX ADK11466;

XX XX

XX 06-MAY-2004 (first entry)

XX DE

XX Human glycogen synthase kinase 3 beta gene.

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

XX KW

ds; gene; cytostatic; cardiovascular; immunosuppressive; nephrotropic;
 antineumatic; aniarthritic; dermatological; antipsoriatic;
 antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;
 cardiovascular disorder; autoimmune disease; glomerulonephritis;
 rheumatoid arthritis; dermatological disorder; psoriasis;

KW inflammatory disorder; malaria; emphysema; alopecia.

XX Homo sapiens.

XX WO2003040301-A2.

XX 15-MAY-2003.

XX 23-OCT-2002; 2002WO-GB0004780.

XX 05-NOV-2001; 2001GB-00026506.

XX 27-NOV-2001; 2001GB-00028384.

XX 11-FEB-2002; 2002GB-00003185.

XX (CYCL-) CYCLACEL LTD.

XX Deak P, Frenz L, Glover D, Midgley C;

XX WPI; 2003-441540/41.

XX P-PSDB; ADK11467.

XX New Drosophila polypeptides and polynucleotides, useful for diagnosing,

XX preventing and/or treating disorders, such as cancer, glomerulonephritis,

XX rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.

XX Example 27; Page 218; 265pp; English.

XX The invention relates to novel Drosophila species DNA sequences and their
 CC encoded proteins with their corresponding human homologues. The proteins
 CC or their encoding polynucleotides are useful in a method of prevention,
 CC treatment or diagnosis of a disease in an individual, and used to
 CC identify a substance capable of binding to the polypeptide or modulating
 CC the function of the polypeptide comprising incubating the polypeptide
 CC with a candidate substance and determining whether the substance binds to
 CC the polypeptide. The compositions are administered to an individual in
 CC need of such treatment. The method of diagnosis, in which the presence or
 CC absence of a polynucleotide is detected in a biological sample, comprises
 CC brining the biological sample containing the nucleic acid such as DNA or
 CC RNA into contact with a probe comprising a fragment of at least 15
 CC nucleotides of the polynucleotide, and detecting any duplex formed
 CC between the probe and nucleic acid in the sample. The method also
 CC comprises providing an antibody capable of binding to the polypeptide,
 CC incubating a biological sample with the antibody to allow the formation
 CC of an antibody-antigen complex, and determining whether antibody-antigen
 CC complex comprising the antibody is formed. The disease comprises a
 CC proliferative disease such as cancer. The antibody or identified
 CC substance is also useful in inhibiting the function of a polypeptide
 CC and/or regulating a cell division cycle function. The diseases also
 CC include cardiovascular disorders, autoimmune diseases such as
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as
 CC malaria, emphysema and alopecia. This sequence represents a human homolog
 CC gene for one of the Drosophila genes of the invention.

XX SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-55e-212 Length: 1389
 Score: 2024.00 Matches: 384
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 97.3% Indels: 0
 DB: 10 Gaps: 0

US-10-733-816-2 (1-394) x ADK11466 (1-1389)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30

DB 40 ATGTGAGGGGGCCAGAACCACTCTCTTTGGGAGAGCTGCAAGCGGTGCAGCGCT 99

QY 31 SerAlaPheGlySerMetIleValSerArgAspIleAspGlySerIleValThrVal 50

DB 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGGACCGCAGCAAGGTGCAACAGTG 159

QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGlnValSerTyrThrAspThrLys 70
 DB 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAAGTCAGCTATACAGACACTAAA 219
 QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
 DB 220 GTGATTGGAAATGGATCATTTGGTGGGTATATCAAGCCAAACTTTGTGATTACGGAGAA 279
 QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
 DB 280 CTGGTCGCCATCAAGAAAGTATTTCAGGACAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
 DB 340 ATGAGAAAGCTAGATCACTCAATAGTCCGATTGGTGTATTCTTCTTCTACTCCAGTGGT 399
 QY 131 GluLysIleAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
 DB 400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 459
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
 DB 460 AGAGTTGCCAGACACTATAGTCCAGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 DB 520 TATATGTATCAGCTGTTCCGAGTTAGCTATATCCATTCCTTTGGAACTCGCATCGG 579
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValIleLysLeuCysAsp 210
 DB 580 GATATTAAACCCGAGAACCTCTTTGGTGGATCCTGTGATACTGCTGTTATTAACAACTCTGTGAC 639
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 DB 640 TTTGGAGTGCAGAGCAGCTGGTCCGAGGAGAACCCATGTTTCGTATATCTGTCTCGG 699
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
 DB 700 TACTATAGGGCACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 DB 760 TGTCTGCTGGCTGTGTGGTGGCTGAGCTGTACTAGGACAACCAATATTTCCAGGGGAT 819
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
 DB 820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGGAACCTCCACAGGGAGCAA 879
 QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
 DB 880 ATCAGAGAAATGAACCCAACTACAGAAATTTAAATTCCTCAAATTAAGGCACATCCT 939
 QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
 DB 940 TGGACTAAGGTCTTCCGACCCCACTCCACCGGAGGCAATTCGACTGTGTAGCCGCTG 999
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
 DB 1000 CTGGAGTATACCAACTGCCCCGACTTACACCACTGGAAGCTTGTGCACATTCATTTTTT 1059
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
 DB 1060 GATGAATTCGGGACCCAAATGTCAAACATCCAAATGGGGGAGACACACCTGCACCTCTC 1119
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
 DB 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTCTTATTCCTCCT 1179
 QY 391 HisAlaArgIle 394
 DB 1180 CATGCTCGGATT 1191

RESULT 5	Query Match:	97.3%	Indels:	0
ADIS6612	DB:	12	Gaps:	0
ID ADIS6612 standard; DNA; 1389 BP.	US-10-733-816-2 (1-394) x ADIS6612 (1-1389)			
XX AC ADIS6612;				
XX DT 22-APR-2004 (first entry)				
XX DE Human polynucleotide probe #1414.				
XX KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;				
XX KW effector-like polypeptide; cancer; immunopathology; neuropathology;				
XX KW drug development; toxicology; carcinogenicity;				
XX KW signalling pathway polypeptide; adrenal gland; bladder; bone;				
XX KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;				
XX KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;				
XX KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.				
XX OS Homo sapiens.				
XX PN US2004010136-A1.				
XX PD 15-JAN-2004.				
XX PF 26-NOV-2002; 2002US-00305720.				
XX PR 30-JAN-1998; 98US-00016434.				
XX PA (INCY-) INCYTE GENOMICS INC.				
XX PI Au-Young J, Seilhamer JJ;				
XX DR WPI; 2004-090520/09.				
XX PT New composition comprising polynucleotide probes, useful as array				
XX PT elements in a microarray for monitoring the expression of target				
XX PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic				
XX PT fragments.				
XX PS Claim 6; SEQ ID NO 1414; 73pp; English.				
XX CC The invention relates to a composition of polynucleotide probes				
XX CC comprising first polynucleotide probes comprising at least a portion of a				
XX CC gene encoding a receptor-like polypeptide, second polynucleotide probes				
XX CC comprising at least a portion of a gene encoding a transducing				
XX CC polypeptide and third polynucleotide probes comprising at least a portion				
XX CC of a gene encoding an effector-like polypeptide. The probes of the				
XX CC composition are useful as array elements in a microarray for monitoring				
XX CC the expression of target polynucleotides. The microarray is useful in the				
XX CC diagnosis and treatment of cancer, an immunopathology or a				
XX CC neuropathology. It can also be used for drug discovery and development,				
XX CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.				
XX CC Microarrays can also be used for monitoring the progression of diseases				
XX CC that may be associated with the altered expression of signalling pathway				
XX CC polypeptides. The composition can also be used to purify a subpopulation				
XX CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile				
XX CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of				
XX CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,				
XX CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or				
XX CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,				
XX CC epilepsy, Alzheimer's disease or depression. This sequence represents a				
XX CC human polynucleotide probe of the invention. Note: The sequence data for				
XX CC this patent did not form part of the printed specification but was				
XX CC obtained in electronic format directly from USPTO at				
XX CC seqdata.uspto.gov/sequence.html.				
XX SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;				
Alignment Scores:				
Pred. No.:	1.55e-212	Length:	1389	
Score:	2024.00	Matches:	384	
Percent Similarity:	100.0%	Conservative:	0	
Best Local Similarity:	100.0%	Mismatches:	0	

QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
 Db 1060 GATGAATTACGGGACCCAAATGTCAAAATCCAAATGGGCGAGACACACCTGCCTCTTC 1119
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
 Db 1120 AACTTACCACTCAAGAACTGTCAAGTAATCCACTCTGGCTACCATCTTATCTCTCT 1179
 QY 391 HisAlaArgile 394
 Db 1180 CATGCTCGGATT 1191
 RESULT 6
 ADR40190
 ID ADR40190 standard; cDNA; 1389 BP.
 XX
 AC ADR40190;
 XX
 DT 18-NOV-2004 (first entry)
 XX Human glycogen synthase kinase 3 beta (GSK3beta) (1521) cDNA.
 DE
 XX
 KW haematological; cytosolic; erythroid; anaemia; erythrocytosis;
 KW bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;
 KW T-cells; neutropenia; gene therapy; human; ss; gene;
 KW glycogen synthase kinase 3 beta; GSK3beta.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 40..1302
 FT /*tag= a
 FT /product= "Human glycogen synthase kinase 3 beta
 FT (GSK3beta) (1521) protein"
 XX
 PN WO2004072242-A2.
 XX
 PD 26-AUG-2004.
 XX
 XX 05-FEB-2004; 2004WO-US003417.
 XX
 PR 05-FEB-2003; 2003US-0445241P.
 PR 18-FEB-2003; 2003US-0448389P.
 PR 20-MAR-2003; 2003US-0456320P.
 PR 03-APR-2003; 2003US-0460279P.
 PR 28-APR-2003; 2003US-0465924P.
 PR 13-MAY-2003; 2003US-0470052P.
 PR 26-AUG-2003; 2003US-0498106P.
 PR 04-SEP-2003; 2003US-0500179P.
 PR 15-SEP-2003; 2003US-0502909P.
 PR 10-OCT-2003; 2003US-0510351P.
 PR 17-OCT-2003; 2003US-0512380P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Kelly LM, Carroll JM, Farlow D, Healy A;
 XX
 XX WPI: 2004-625850/60.
 DR P-PSDB; ADR40191.
 DR
 XX Identifying a compound capable of treating a hematological disorder
 FT comprises combining a compound to be tested with a polypeptide related
 PT with the disorder under conditions suitable for binding of the test
 PT compound to the polypeptide.
 XX
 PS Disclosure; SEQ ID NO 71; 321pp; English.
 XX
 CC The invention relates to a novel method for identifying a compound
 CC capable of treating a hematological disorder which comprises combining a
 CC compound to be tested with a specific polypeptide under conditions
 CC suitable for binding of the test compound to the polypeptide. The method
 CC of the invention has haematological and cytostatic applications and may
 CC be useful for identifying compounds for treating a haematological

CC disorder associated with erythroid cells e.g. anaemia and erythrocytosis,
 CC bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and
 CC thrombosis or B-cells and T-cells e.g. neutropenia. The compounds
 CC identified may be utilised during gene therapy procedures. The current
 CC sequence is that of a human haematological disorder-related cDNA of the
 CC invention.
 XX
 SQ Sequence 1389 BP; 402 A; 326 C; 326 G; 335 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1-55e-212 Length: 1389
 Score: 2024.00 Matches: 384
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 97.3% Indels: 0
 DB: 13 Gaps: 0
 US-10-733-816-2 (1-394) x ADR40190 (1-1389)
 QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
 Db 40 ATGTCAGGCGCGCCAGAACCACTCTTTGCGAGAGCTGCAAGCGGTGCAGACGCT 99
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
 Db 100 TCAGCTTTTGGCAGCATGAAGATTAGCAGACAGGACGCGCAAGGTGACAACAGTG 159
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
 Db 160 GTGGCAACTCTTGGCAGGCTCCAGACAGGCCACAGAGTCTAGCTATACAGACACTAA 219
 QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
 Db 220 GTGATTGGAAATGGATCAATTTGGTGTGTATATCAAGCCAAACTTCTGATTGAGGAA 279
 QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
 Db 280 CTGGTCGCCATCAAGAAAGATTTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
 Db 340 ATGAGAAAGCTAGATCACTGTAACTAGTCCGATTGGGTATTCTTCTACTCCAGTGT 399
 QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
 Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTCGGAACAGTATAC 459
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
 Db 460 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGCAAGTTG 519
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 Db 520 TATATGATCAGCTGTTCGAGTTAGCTATATCAATCTCTTGGAACTCTGCCATCGG 579
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
 Db 580 GATATTAAACCGCAGAACCTCTTGTGGATCCTGTACTGTCTGTATTTAAACTCTGTGAC 639
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 Db 640 TTTTGAAGTGCAAAGCAGCTGGTCCGAGGAGAAACCAATGTTTCGTATATCTCTTCGG 699
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
 Db 700 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 759
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 Db 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTTCCAGGGAT 819
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290

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Db      820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGTCTCTGGAACTCCCAACAGGAGCAA 879
Qy      291 ILAArgGluMetAenProAenTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
      |||||
Db      880 ATCAGAGAAATGAACCCCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
Qy      311 TTPThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
      |||||
Db      940 TGGACTAAGGCTCTCCGACCCCGAACTCCACCGAGGCAATTCACATGTGTAGCCGTCG 999
Qy      331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
      |||||
Db      1000 CTGGAGTATACCAACTGCGCGACTAACCACTGGAAGCTGTGTGCACATTCATTTTT 1059
Qy      351 AspGluLeuArgAepProAenValLysHisProAenGlyArgAepThrProAlaLeuPhe 370
      |||||
Db      1060 GATGAATTACGGGACCCCAATGTCAAAATCCAAATGGGCGAGACACACCTGCACCTTTC 1119
Qy      371 AsnPheThrThrGlnGluLeuSerSerAenProLeuAlaThrIleLeuIleProPro 390
      |||||
Db      1120 AACTTACCACCTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCCTTATTCCTCT 1179
Qy      391 HisAlaArgIle 394
      |||||
Db      1180 CATGCTCGGATT 1191

RESULT 7
ADBS3390
ID      ADBS3390 standard; DNA; 1525 BP.
XX      AC      ADBS3390;
XX      DT      04-DEC-2003 (first entry)
XX      DE      Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3932.
XX      KW      toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX      KW      toxicity marker; toxicity progression; drug screening;
XX      KW      primary rat hepatocyte toxicity modelling; gene; ds.
XX      OS      Rattus norvegicus.
XX      PN      WO2003065993-A2.
XX      PD      14-AUG-2003.
XX      PF      04-FEB-2003; 2003WO-US003482.
XX      PR      04-FEB-2002; 2002US-0353171P.
XX      PR      13-MAR-2002; 2002US-0363534P.
XX      PR      08-APR-2002; 2002US-0370248P.
XX      PR      10-APR-2002; 2002US-0371134P.
XX      PR      10-APR-2002; 2002US-0371135P.
XX      PR      10-APR-2002; 2002US-0371150P.
XX      PR      11-APR-2002; 2002US-0371413P.
XX      PR      13-APR-2002; 2002US-0373601P.
XX      PR      19-APR-2002; 2002US-0373602P.
XX      PR      22-APR-2002; 2002US-0374139P.
XX      PR      08-MAY-2002; 2002US-0378370P.
XX      PR      09-MAY-2002; 2002US-0378652P.
XX      PR      09-MAY-2002; 2002US-0378653P.
XX      PR      09-MAY-2002; 2002US-0378655P.
XX      PR      09-JUL-2002; 2002US-0394230P.
XX      PR      09-JUL-2002; 2002US-0394253P.
XX      PR      04-SEP-2002; 2002US-0407688P.
XX      PR      28-JAN-2003; 2003US-0442900P.
XX      (GENE-) GENE LOGIC INC.
XX      PA      Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
XX      PI      Elashoff M;
XX      WPI; 2003-731472/69.
XX      , DR
```

```
XX      XX      Claim 44; SEQ ID NO 3932; 874pp; English.
XX      CC      The present invention describes a method for determining whether a
XX      CC      compound induces a toxic effect on a tissue or cell. The method comprises
XX      CC      preparing a gene expression profile of a tissue or cell sample exposed to
XX      CC      the compound, and comparing the gene expression profile to a database
XX      CC      comprising data or information on the Tox mean and non-Tox mean value.
XX      CC      The method is useful for predicting or identifying at least one toxic
XX      CC      effect, particularly hepatotoxicity, of a test or unknown compound. The
XX      CC      genes listed in the specification are useful as diagnostic or toxicity
XX      CC      markers for the prediction or identification of the physiological state
XX      CC      of tissue or cell sample that has been exposed to a compound, or to
XX      CC      identify or predict the toxic effects of a compound or an agent. These
XX      CC      may also be used as markers for monitoring toxicity progression or for
XX      CC      drug screening. The present sequence represents a primary rat hepatocyte
XX      CC      toxicity modelling related gene sequence from the present invention.
XX      SQ      Sequence 1525 BP; 459 A; 372 C; 351 G; 343 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,75e-211      Length:      1525
Score:      2015.00      Matches:      386
Percent Similarity:      98.0%      Conservative:      0
Best Local Similarity:      98.0%      Mismatches:      2
Query Match:      96.8%      Indels:      6
DB:      10      Gaps:      1

US-10-733-816-2 (1-394) x ADBS3390 (1-1525)
Qy      7      GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
      |||||
Db      110 GAAGGAAAGGTGAATCGAGAGAGCCATCATCTGCGGGCGACCGAGAACCACTCTCTT 169
Qy      21      AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
      |||||
Db      170 GCGGAGAGCTGCAAGCCAGTCGACGAGCCCTTCAGCTTTTGGTAGCATGAAAGTTAGCAGA 229
Qy      41      AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60
      |||||
Db      230 GATAAGAGATGGCAGCAAGGTAAACACAGTGTGGCAACTCTCTGGACAGGGTCTCTGACAGG 289
Qy      61      ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
      |||||
Db      290 CCACAGGAAGTCAGTTACACAGACACTAAAGTCATTGGAAATGGGTCACTTTGGTGTGTA 349
Qy      81      TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
      |||||
Db      350 TATCAAGCCAAACTTTGTGACTCAGGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409
Qy      101      LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
      |||||
Db      410 AAGCGATTTAAGAACCCGAGAGCTCCAGATCATGAGAAGGCTAGATCACTGTAAACATAGTC 469
Qy      121      ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
      |||||
Db      470 CGATTGGGTATTTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACCTTAACCTG 529
Qy      141      ValLeuAspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLys 160
      |||||
Db      530 GTGCTGGACTATGTTCGGGAAACAGTGTACAGAGTCCGCCAGACACTATAGTCGAGGCCAAG 589
Qy      161      GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
      |||||
Db      590 CAGACACTCCCTGTGATCTATGTCAGAGTTGATATGTACAGCTGTTCAGAAAGTCTAGCC 649
Qy      181      TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
      |||||
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XX      PT      Determining if a compound induces a toxic effect on a tissue or cell, for
XX      PT      identifying hepatotoxic compounds, comprises comparing a gene expression
XX      PT      profile of a tissue or cell sample to a database of Tox mean and non-Tox
XX      PT      mean values.
XX      PS      Claim 44; SEQ ID NO 3932; 874pp; English.
XX      CC      The present invention describes a method for determining whether a
XX      CC      compound induces a toxic effect on a tissue or cell. The method comprises
XX      CC      preparing a gene expression profile of a tissue or cell sample exposed to
XX      CC      the compound, and comparing the gene expression profile to a database
XX      CC      comprising data or information on the Tox mean and non-Tox mean value.
XX      CC      The method is useful for predicting or identifying at least one toxic
XX      CC      effect, particularly hepatotoxicity, of a test or unknown compound. The
XX      CC      genes listed in the specification are useful as diagnostic or toxicity
XX      CC      markers for the prediction or identification of the physiological state
XX      CC      of tissue or cell sample that has been exposed to a compound, or to
XX      CC      identify or predict the toxic effects of a compound or an agent. These
XX      CC      may also be used as markers for monitoring toxicity progression or for
XX      CC      drug screening. The present sequence represents a primary rat hepatocyte
XX      CC      toxicity modelling related gene sequence from the present invention.
XX      SQ      Sequence 1525 BP; 459 A; 372 C; 351 G; 343 T; 0 U; 0 Other;
```


QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
 DB 473 CTGGTCGCCATCAAGAAGATTTCGAGCAACAGAGATTTAAGAAATCGAGAGCTCCAGATC 532
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
 DB 533 ATGAGAAAGCTAGATCACTGTACATAGTCCGATTGGCTATTCTTCTACTCAGTGGT 592
 QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
 DB 593 GAGAAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGAAACAGTATAC 652
 QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
 DB 653 AGAGTTGCCACAGACTATAGTCCAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 712
 QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 DB 713 TATATGATCAGCTGTTCCGAGTTTAGCTTATATCCATTCCTTTGGATCTCCATCGG 772
 QY 191 AspLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
 DB 773 GATATTAAACCGCAGAACCTCTTGTGGATCCTGATACCTGCTGTATTAAACTCTGTGAC 832
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 DB 833 TTTTGAAGTCAAGACGCTGGTCCGAGGAGAACCAATGTTTCGTATATCTGTCTCGG 892
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyValThrAspTyrThrSerSerIleAspVal 250
 DB 893 TACTATAGGCACACAGATTTGATCTTTGGAGCCACTGATTATACCTCTAGTAGATGTA 952
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 DB 953 TGGTCTGCTGCTGTGTGGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGAT 1012
 QY 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
 DB 1013 AGTGGTGTGGATCAGTTGGTGAATAATCAAGTCTCTGGGAACCTCCAAAGGAGCA 1072
 QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
 DB 1073 ATCAGAGAAATGAACCCAACTACACAGATTTAAATTCCTCAAAATTAAGGCACATCCT 1132
 QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
 DB 1133 TGGACTAAGTCTTCCGACCCCGACTCCACCGAGGCAATTCGACTGTGTAGCCGCTCG 1192
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
 DB 1193 CTGGAGTATACCAACTGCCCGACTAACCACTGGAAGCTTGTGCACATTCATTTT 1252
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
 DB 1253 GATGAATTAAGGACCCCAATGTCAAACTACCAAAATGGGCGAGACACACCTGCACCTTC 1312
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
 DB 1313 AACTTACCACTCAGAACTGTCAAGTAACTCCACTCTGGCTACCATCTTATCTCTCT 1372
 QY 391 HisAlaArgIle 394
 DB 1373 CATGCTCGGATT 1384
 RESULT 12
 ID ABV30267
 XX ABV30267 standard; cDNA; 1815 BP.
 AC ABV30267;
 XX
 XX
 DT 16-SEP-2002 (first entry)
 XX

DE Human prostate expression marker cDNA 30258.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US0005171.

XX 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6569; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 1815 BP; 528 A; 406 C; 420 G; 458 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.: 3,79e-211 Length: 1815
 Score: 2013.00 Matches: 383
 Percent Similarity: 99.7% Conservative: 0
 Best Local Similarity: 99.7% Mismatches: 1
 Query Match: 96.7% Indels: 0
 DB: 5 Gaps: 0

US-10-733-816-2 (1-394) x ABV30267 (1-1815)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30

DB 325 AYTGTAGGGGGGCCAGAACCCACTCTTTTGGAGAGCTGCAAGCGGTGACAGCCT 384

QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50

DB 385 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACACAGGACGCGCAAGGTGACACAGTG 444

QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70

DB 445 GTGGCAACTCTCTGGGCGAGGTCCAGACAGGCCCAAGAAAGTACGATATACAGACCTAAA 504

QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90

DB 505 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGTTTCAGGAGAA 564

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QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
DB 565 CTGGTCGCCATCAAGAAGATTATGACGAGCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 624
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
DB 625 ATGGAAGAAGCTAGATCACTGTAACATAGTCGGATTGGGTATTCTTCTACTCCAGTGGT 684
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
DB 685 GAGAAGAAGATGAGGTCTATCTTAATCTGGTCTGACATATGTTCCGGAACAGTATAC 744
QY 151 ArgValAlaAlaArgHisTyrSerArgAlaLysGluThrLeuProValIleTyrValLysLeu 170
DB 745 AGAGTTGCCAGACACTATATGTCGAGCCAAACACAGCGCTCCCTGTGATTTATGTCAAGTTG 804
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 805 TATATGTATCAGCTGTTCCGAAGTTTAGCCTATATCCATTCCTTTGGAACTCGCCATCGG 864
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
DB 865 GATATTAAACCGCAGAACCTCTTGTGGATCCTGATACCTGCTGTATTAAAACTCTGTGAC 924
QY 211 PheGlySerAlaLysGlnLeuValAlaTqGlyGluProAsnValSerTyrIleCysSerArg 230
DB 925 TTTGGAAAGTCAAGACAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCTCGG 984
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
DB 985 TACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTACTATAGATGA 1044
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
DB 1045 TGGTCTGCTGGCTGTGTGGTGGCTGAGCTGTACTAGGCAACCAATATTTCAGGGGGAT 1104
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
DB 1105 AGTGGTGTGATCAGTTGGTAGAAATTAATCAAGTCTCTGGAACTCCAAACAGGGAGCAA 1164
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
DB 1165 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 1224
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
DB 1225 TGGACTAAGGTCTTCCGACCCGAACTCCACCGGAGGCAATTGCACCTGTGTAGCCGCTG 1284
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
DB 1285 CTGGAGTATACCAACTGCCCGACTAACCCACTGGAAGCTGTGTGCACATTTCAATTTTT 1344
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
DB 1345 GATGAATACGGGACCCCAATGTCAAACTACCAATAGGCGAGACACACCTGCACCTCTTC 1404
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
DB 1405 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCCT 1464
QY 391 HisAlaArgIle 394
DB 1465 CATGCTCGGATT 1476
RESULT 13
ID AEA62868 standard; DNA; 1474 BP.
AC AEA62868;
XX
XX 25-AUG-2005 (first entry)
XX
XX Rat glycogen synthase kinase 3-beta (GSK3-beta) DNA sequence - SEQ ID 17.
```

```
XX antisense therapy; bone; bipolar disorder; neuroleptic; mania; antimanic;
KW Alzheimers disease; neuroprotective; nootropic; diabetes; antidiabetic;
KW leukopenia; immunostimulant; hyperproliferation; cytostatic;
KW glycogen synthase kinase 3-beta; GSK3-beta; ds.
OS Rattus norvegicus.
XX
PN W02005054518-A2.
XX
PD 16-JUN-2005.
XX
XX 06-DEC-2004; 2004WO-US041019.
XX
XX 04-DEC-2003; 2003US-0527172P.
PR 04-DEC-2003; 2003US-0527173P.
PR 04-DEC-2003; 2003US-0527174P.
PR 04-DEC-2003; 2003US-0527370P.
PR 04-DEC-2003; 2003US-0527397P.
PR 04-DEC-2003; 2003US-0527420P.
PR 03-DEC-2004; 2004US-00004762.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett FC, Butler WM, Dean NM, Dobie KW, Finger J, Jain R;
PI McKay R, Monia BP, Myers K;
XX WPI; 2005-435410/44.
DR
XX Novel oligomeric compound having nucleobases targeted to bone growth
PT modulator nucleic acid, and inhibiting expression of bone growth
PT modulator e.g., sclerostin, useful for inhibiting expression of bone
PT growth modulator in animal.
XX
XX Example 4; SEQ ID NO 17; 357pp; English.
XX
XX The invention comprises oligomeric compounds which are targeted to a
XX nucleic acid molecule encoding a bone growth modulator chosen from
XX dickkopf-1 (DKK-1), glycogen synthase kinase 3-beta, (GSK3-beta), s-
XX frizzled-related protein 1 (sFRP-1), sclerostin, transducer of ERBB1, and
XX arc-c. The oligomeric compound of the invention is capable of inhibiting
XX the expression of the bone growth modulator. The oligomeric compound of
XX the invention is useful for inhibiting the expression of a bone growth
XX modulator in a biological fluid, cell or tissue. The oligomeric compound
XX of the invention is further useful in the treatment of bipolar disorder,
XX mania, Alzheimer's disease, diabetes, leukopenia, sclerosteosis, and
XX hyperproliferative disorders. The present nucleic acid represents a rat
XX GSK3-beta DNA sequence.
XX
XX Sequence 1474 BP; 436 A; 365 C; 341 G; 332 T; 0 U; 0 Other;
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Pred. No.: 3,56e-211 Length: 1474
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Best Local Similarity: 97.7% Mismatches: 2
Query Match: 96.7% Indels: 6
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QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
DB 145 GCGGAGAGCTGCAAGCCAGTCAGTCAGAGCCCTTCAGCTTTTGTAGCATGAAGTTAGCAGA 204
QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
DB 205 GATAAAGATGGCAGCAAGGTAAACCAAGTGTGTGGCAACTCTCTGGACAGGGGTCTCTGACGG 264
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Db 93 TCAGCTTTTGGTAGCTGAAGTTAGCAGAGATAAAGATGCGCAGCAAGGTAAACACAGTA 152
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 153 GTGGCACTCTCGCCAGGCTCTGACAGGCCACAGGAAGTCAGTTATATACAGACAGAAA 212
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 213 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCTGGAGAA 272
Qy 91 LeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 273 CTGGTCCCATCAAGAAAGTTCTACAGCACAAGGATTTAAGAACCGAGAGCTCCAGATC 332
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 333 ATGAGAAAGCTAGACCACTGTAACTAGTCCGACTCGGTTATTTCTTACTACTCGAGTGT 392
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 393 GAGAAGAAGATGAGTCTACCTTAACCTGGTGTGACTATGTTCGGAGACAGTGTAC 452
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 453 AGAGTCCCCAGACACTATAGTCGAGCCAGACAGACACTCCCTGTGATCTATGTCAGATTG 512
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 513 TATATGTATCAGCTGTTTCAGAGTCTAGCTATATCATTCCTTTGGAACTCGCCATCGA 572
Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 573 GACATTAAACACACAGAACCTCTGTGGATCCTGATACAGCTGTATTAAAACTCTGTGAC 632
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 633 TTTGGAAAGTCAAGACAGCTGTGTCGAGGAGAGCCCAATGTTTCATATATCTGTCTCGG 692
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 693 TACTACAGGCGCACAGAGTTGATCTTTGGAGCCACTGATTACAGCTCCAGTATAGATGTA 752
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 753 TGGTCTCAGGCTGTGTGTGGCTGAATGTGTCTAGGCAACCAATATTTCTCGGGGAC 812
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 813 AGTGCTGTGATCATGTTGGTGGAAATTAAGTCTCTAGAACACCAACAGGGAGCAA 872
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 873 ATTAGAGAAATGAACCCAAATTTATACAGAAATTCCTCAAAATCAAGGCACATCCT 932
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 933 TGGCAAAAGGTCTTCCGCGCCCGAACTCCACAGAGGCAATTTGCACGTGTGCGCGCTG 992
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 993 CTGGAGTACACACTACGCGCCGGCTAACCACTGGAGCTGTGGACATTCATTTTTC 1052
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1053 GATGAATTGCGGACCCCAATGTCAAACTACCAATGGCGGAGACACACCTGCACCTTTC 1112
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
Db 1113 AACTTTTACCCTCAAGAACTGTCAAGTAACCCCTCTGGCCACCATCTTATCCCTCCA 1172
Qy 391 HisAlaArgIle 394
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Db 1173 CATGCTCGGATT 1184
RESULT 15
AAQ67458
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XX AAQ67458;
AC AAQ67458;
XX 25-MAR-2003 (revised)
DT 21-APR-1995 (first entry)
XX Codes tau-protein kinase I (TPK-I), Alzheimer's disease.
XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease; ds.
OS Homo sapiens.
XX Key Location/Qualifiers
FT mat_peptide 616..1885
FT /*tag= a
XX EP616032-A2.
XX 21-SEP-1994. 94EP-00103057.
XX 01-MAR-1994;
XX 02-MAR-1993; 93JP-00041160.
XX 22-MAR-1993; 93JP-00085143.
XX 02-AUG-1993; 93JP-00191246.
XX (MITU) MITSUBISHI KASEI CORP.
PA (MITU) MITSUBISHI CHEM CORP.
XX Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A;
Sato S;
WPI; 1994-287181/36.
DR P-PSDB; AAR61326.
XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-protein providing means for prevention and treatment of Alzheimer's disease.
XX Claim 4; Page 14; 30pp; English.
XX AAQ67458 codes for a newly isolated tau-protein kinase I enzyme (TPK-1), shown in AAR61326 (compare to rat AAR61327). The cDNA was cloned from a rat fetus brain cDNA library, and was expressed in insect cells. TPK-I acts specifically on tau-protein, which is thought to be involved in Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped that the characterisation of TPK-I may lead to development of new agents for the prevention and therapy of these diseases. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 2088 BP; 656 A; 452 C; 434 G; 546 T; 0 U; 0 Other;
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Query Match: 96.6% Indels: 0
DB: 2 Gaps: 0
US-10-733-816-2 (1-394) x AAQ67458 (1-2088)
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Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
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Job time : 1262 secs

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Qy      71 valileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
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Qy      91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
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Qy      111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
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Qy      171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
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Qy      191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
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Qy      211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db      1216 TTTGGAAGTGCAGAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 1275
Qy      231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
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Qy      251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db      1336 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACAACCAATATTTCCAGGGGAT 1395
Qy      271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
Db      1396 AGTGGTGTGGATCAGTTGGTAGAATAATCAAGGTCTCTGGGAACCTCAACAAGGGAGCAA 1455
Qy      291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db      1456 ATCAGAGAAATGAACCCAACTACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 1515
Qy      311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
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Qy      331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
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Qy      351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
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Qy      371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
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Qy      391 HisAlaArgIle 394
Db      1756 CATGCTCGGATT 1767
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GenCore version 5.1.9
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Run on: September 17, 2006, 10:54:31 ; Search time 406 Seconds
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Title: US-10-733-816-2

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Delop 6.0 , Delext 7.0

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Maximum Match 100%

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SUMMARIES

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2	2024	97.3	1389	3	US-09-016-434-1414
3	2015	96.8	1972	2	US-08-602-264A-2
4	2015	96.8	1972	3	US-08-461-018A-2
5	2015	96.8	1972	3	US-09-216-958-2
6	2010	96.6	2088	2	US-08-602-264A-1
7	2010	96.6	2088	3	US-08-461-018A-1
8	2010	96.6	2088	3	US-09-216-958-1

9	1609	77.3	1952	3	US-09-566-921-24	Sequence 24, Appl
10	1609	77.3	2154	3	US-09-488-856A-3	Sequence 3, Appl
11	1245	59.8	1636	3	US-09-578-194-6	Sequence 6, Appl
12	1244.5	59.8	1814	3	US-09-347-801-9	Sequence 9, Appl
13	1244.5	59.8	1814	3	US-09-854-731-9	Sequence 9, Appl
14	1240	59.6	1673	3	US-09-347-801-15	Sequence 15, Appl
15	1240	59.6	1673	3	US-09-854-731-15	Sequence 15, Appl
16	1165.5	56.0	1429	3	US-09-347-801-13	Sequence 13, Appl
17	1165.5	56.0	1429	3	US-09-854-731-13	Sequence 13, Appl
18	1001.5	48.1	1185	3	US-09-248-796A-4396	Sequence 4396, Ap
19	788	37.9	479	2	US-08-602-264A-13	Sequence 13, Appl
20	788	37.9	479	3	US-08-461-018A-13	Sequence 13, Appl
21	788	37.9	479	3	US-09-216-958-13	Sequence 13, Appl
22	674	32.4	1236	3	US-09-248-796A-4397	Sequence 4397, Ap
23	622	29.9	12394	3	US-09-488-856A-10	Sequence 10, Appl
24	518.5	24.9	438	3	US-09-270-767-11493	Sequence 11493, A
25	485	23.3	3823	3	US-09-949-016-4276	Sequence 4276, Ap
26	480	23.1	1158	3	US-09-949-016-4906	Sequence 4906, Ap
27	478.5	23.0	1161	3	US-09-023-655-1373	Sequence 1373, Ap
28	478.5	23.0	1161	3	US-09-949-016-181	Sequence 181, App
29	478.5	23.0	1825	3	US-09-620-312D-313	Sequence 313, App
30	472.5	22.7	1866	3	US-08-909-742-1	Sequence 1, Appl
31	472.5	22.7	1866	3	US-09-417-197-38	Sequence 38, Appl
32	472.5	22.7	1896	3	US-09-412-289-1	Sequence 1, Appl
33	466	22.4	1544	2	US-08-837-593-1	Sequence 1, Appl
34	464.5	22.3	1875	3	US-09-417-197-56	Sequence 56, Appl
35	460.5	22.1	1296	3	US-09-949-016-2154	Sequence 2154, Ap
36	460.5	22.1	2213	3	US-09-023-655-1037	Sequence 1037, Ap
37	459	22.1	1635	3	US-09-417-197-112	Sequence 112, App
38	458.5	22.0	1725	3	US-09-623-034-1	Sequence 1, Appl
39	457	22.0	1467	2	US-08-176-820A-3	Sequence 3, Appl
40	457	22.0	1467	2	US-08-463-862-3	Sequence 3, Appl
41	457	22.0	1467	2	US-08-461-985-3	Sequence 3, Appl
42	457	22.0	1467	2	US-08-458-887-3	Sequence 3, Appl
43	457	22.0	1467	3	US-08-932-787B-3	Sequence 3, Appl
44	457	22.0	1467	3	US-08-932-012C-3	Sequence 3, Appl
45	457	22.0	1467	3	US-08-888-818C-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-489-765A-3
; Sequence 3, Application US/09489765A
; Patent No. 6323029
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES
; FILE REFERENCE: RTS-0124
; CURRENT APPLICATION NUMBER: US/09/489,765A
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-09-489-765A-3

Alignment Scores:			
Pred. No.:	1.67e-237	Length:	1389
Score:	2024.00	Matches:	384
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	97.3%	Indels:	0
DB:	3	Gaps:	0
US-10-733-816-2 (1-394) x US-09-489-765A-3 (1-1389)			

QY 11 MetSerGlyArgProArgThrThrSerPheAlaCysSerCysValGlnGlnPro 30
Db 40 ATGTGAGGGGGCCAGAACCCCTCTTTGGGAGAGCTGCAAGCCGGTGCAGACGCT 99
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGAGCGGCGCAGCAAGGTGACACAGTG 159
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGCGCCACAAGAGTCCAGCTATACAGACCTAAA 219
QY 71 ValIleGlySerGlySerPheGlyValValTyrGlnAlaLysLysCysAspSerGlyGlu 90
Db 220 GTGATTGGAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAA 279
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCCCATCAAGAAAGTATTGCAGACAGAGATTTAAGATCGAGAGCTCCAGATC 339
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCACTGTAACTAGTCGATTCGATTCGATTCCTTCTACTCCAGTGT 399
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAGAAGATGAGGTCTATCTTAATCTGTGTGCTGAGATGTTCGGAACAGTATAC 459
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 519
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGATATCAGCTGTTCGGAAGTTTAGCCCTATATCCATTCCTTTGGAATCTGCATCGG 579
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGCAGAACCTCTTGTGGATCCCTGATATCTGTGATTTAAATCTCTGTGAC 639
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 640 TTTGGAAGTGCNAAGCAGCTGTTCGAGAGAACCCCAATGTTTCGTATATCTGTTCCTCGG 699
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 700 TACTATAGGCACCCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 759
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTCTGGCTGTGTGTGGTGTGAGCTGTACTAGGACCAACCAATATTTCAGGGGAT 819
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 820 AGTGGTGTGATCAGTTGGTAGAATATATCAGGTCTCTGGAACTCCACAGGAGCAAA 879
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 880 ATCAGAGAAATGAACCCCAACATACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 940 TGGACTAAGGTCTTCCAGCCCGCAACTCCACCGGAGGCAATTCACACTGTGTAGCCGCTG 999
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1000 CTGGAGTATACCAACTGCCCGACTAACCACTGGAGAGTCTGGACATTCATTTT 1059
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1060 GATGAATTACGGGACCCAAATGTCAAAATGTCAAAATGGCGGAGACACACCTGCACTCTTC 1119

QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
Db 1120 AACTTACCACCTCAGAACTGTCAAGTATCCACTCTGGCTACCATCTTATTCCTCT 1179
QY 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191
RESULT 2
US-09-016-434-1414
; Sequence 1414, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9529236
; US-09-016-434-1414
Alignment Scores:
Pred. No.: 1.67e-237 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 3 Gaps: 0
US-10-733-816-2 (1-394) x US-09-016-434-1414 (1-1389)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaCysSerCysValGlnGlnPro 30
Db 40 ATGTGAGGGGGCCAGAACCCCTCTTTGGGAGAGCTGCAAGCCGGTGCAGACGCT 99
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACAGAGCGGCGCAGCAAGGTGACACAGTG 159

QY 51 ValalaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGTGCAGTATACAGACACTAAA 219
QY 71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCyAspSerGlyGlu 90
Db 220 GTGATTGGAAATGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTCAGGAGAA 279
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAGATTATGCAGACACAGAGATTTAAGATTCAGAGCTCCAGATC 339
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCACTGTAACATAGTCGATGCGTTGCTTATTTCTTCTCAGTGGT 399
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 459
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACTATATGTCGAGCCAAACAGACGCTCCCTGTGATTATGTCAGTTG 519
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGTATCATGCTGTTCCGAAGTTTAGCCATATATCCATTCCTTTGGAATCTGCCATCG 579
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGGAGAACCTCTTGTGGATCCGTATCTGCTGATTAAACACTCTGGAC 639
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 640 TTTGGAAGTCCAAAGCAGCTGCTCCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTCG 699
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 700 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT 819
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 820 AGTGGTGTGATCAGTTGGTAGAAATATCAAGTCTCTGGGAATCCCAACAGGGAGCAA 879
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 880 ATCAGAGAAATGAACCCAAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 940 TGGACTAAGGTCTTCCGACCCCGAACCTCCACCGAGGCAATTCGACTGTGTAGCCGCTG 999
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1000 CTGGAGTATACCAACTGCCGACTAACCACTGGAAGCTTGTGCACATTCATTTTTT 1059
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1060 GATGAATTACGGGACCCAAATGTCAACATCCAAATGGCGGAGACACACCTGCACCTCTC 1119
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCACTTATTCCTCCT 1179
QY 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191

RESULT 3

US-08-602-264A-2
; Sequence 2, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: rat
US-08-602-264A-2

Alignment Scores:
Pred. No.: 3,82e-236 Length: 1972
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: 2 Gaps: 1

US-10-733-816-2 (1-394) x US-08-602-264A-2 (1-1972)

QY 7 GluGlyGlyGly-----MetSerGlyValArgProArgThrThrSerPhe 20
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QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
Db 170 GCGGAGAGCTGCAAGCCAGTCGAGAGCCCTTCAGCTTTTGTAGCATGAAAGTTAGCAGA 229
QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
Db 230 GATAAAGATGGCAGCAAGGTAAACACAGATGGTGGCAACTCTCTGCAGAGGGTCTCTGACAG 289
QY 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
Db 290 CCAGGAAGTCAAGTTACACAGACACTAAAGTCAATTGGGAAATGGGTCAATTGGTGTGGTA 349

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Db 350 TATCAAGCCAAACTTTGTGACTCAGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409
QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
Db 410 AAGGATTTAAGAACCCAGAGACTCCAGATCATGAGAAGCTAGATCACTGTAAACATAGTC 469
QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
Db 470 CGATTGGGTATTTCTTCTACTCGAGTGGCAGAGAAAGATGAGGTCTACCTTAACTG 529
QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
Db 530 GTGCTGGACTATGTTCCGGAACACAGTGTACAGAGTCGCCAGACACTATAGTCGAGCCAAG 589
QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
Db 590 CAGACATCCCTGTGATCTATGTCNAGTTGTATATGTACCAGCTGTTTCAGAAGTCTAGCC 649
QY 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
Db 650 TATATCCATTCTTTGGGATCTGCCATCGAGACATTAAACCCACAGAACCTCTTGCTGGAT 709
QY 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
Db 710 CCTGATACAGCTGATTAAACATCTGCGACTTTGGAAAGTGCAAGCAGCTGGTCCGAGGA 769
QY 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
Db 770 GAGCCCAATGTTTCATATATCTGTTCTCGTACTACAGGGCCACGAGAGCTGATCTTTGGA 829
QY 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
Db 830 GCCACCGATTACAGCTCTAGTAGATGTTGTGCTCGAGCTGTGTGTTGGCTGAATTG 889
QY 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 280
Db 890 TTGCTAGGACAAACAATTTCTCTGGGGACAGTGTGTGATCAGTTGGTGGAAATAATA 949
QY 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300
Db 950 AAGTCTCTAGAACACCAACAGGAGCAATATAGAGAAATGAACCCAAATATATACGAA 1009
QY 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320
Db 1010 TTCAAAATTCCTCCCAATCAAGGCACATCTTTGGACGAAGTCTTTTCGGCCCGCAACTCCA 1069
QY 321 ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340
Db 1070 CCAGAGCAATTCGCACCTGTGTAGCCGTCTCTGTGAGTACAGCGGACCGCCCGGCTAAAC 1129
QY 341 ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHis 360
Db 1130 CCAGTGAAGCTGTGCACATTCATTTTGTGAAATACGGGACCCCAATGTCAACTA 1189
QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
Db 1190 CCAATGGCGGAGACACACCTGCCCTCTCAACTTTTACCACCTCAAGAACTGTCAAGTAAC 1249
QY 381 ProProLeuAlaThrIleLeuIleProProHisAlaArgIle 394
Db 1250 CCACCTCTGGCCCACTCTTATCCCTCTCACGCTCGGATT 1291
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RESULT 4

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US-08-461-018A-2
; Sequence 2, Application US/08461018A
; Patent No. 6071694
; GENERAL INFORMATION:
; APPLICANT: AKIHIKO TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
```

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; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; US-08-461-018A-2
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Alignment Scores:
Pred. No.: 3,82e-236 Length: 1972
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: 3 Gaps: 1
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US-10-733-816-2 (1-394) x US-08-461-018A-2 (1-1972)

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QY 7 GluGlyGlyGly-----MetSerGlyValArgProArgThrThrSerPhe 20
Db 110 GAAGGAAAGGTGAATCGAAGAGGCCATCATGTGGGGCGACGAGAACCACTCTCTTT 169
QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
Db 170 GCGGAGAGCTGCAAGCCAGTCAGTCAGAGCCTTCAGCTTTTGTAGCATGAAGTAGCAGA 229
QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
Db 230 GATAAAGATGGCAAGAGGTAACACACAGTGTGGCAACTCTCGACAGGGTCTCTGACAGG 289
QY 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
Db 290 CCACGGAAGTCAGTTACACAGACACTAAAGTCAATTGGGAATGGTCACTTTGGTGTGTA 349
QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
Db 350 TATCAAGCCAAACTTTGTGACTCAGAGAACTGGTGCCCATCAAGAAAGTTCTTCAGGAC 409
QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
Db 410 AAGCGATTTAAGAACCCAGAGACTCCAGATCATGAGAAGCTAGATCACTGTAAACATAGTC 469
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QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
DB 470 CGATTGGCGTATTTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACTCTTAACCTG 529
QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
DB 530 GTGCTGGACTATGTTCCGGAACAGTGTACAGAGTCCGACACATATAGTCTGAGCCAG 589
QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
DB 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATACAGCTGTTCAGAACTAGACC 649
QY 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
DB 650 TATATCCATTCCTTTGGATCTGCCATCGACATTAACACACAGACCTCTTCTGGAT 709
QY 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
DB 710 CCTGATACAGCTGTATTAAACTCTGGACTTTGGAAGTGCAGAGCTGCTCCGAGGA 769
QY 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
DB 770 GAGCCCAATGTTTCATATATCTGTCTCGGTACTACAGGCGACAGAGCTGATCTTTGGA 829
QY 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
DB 830 GCCACCGATTACAGCTCTAGTATAGATGTATGGTCTGCAGCGCTGTGTGTGGCTGAATTG 889
QY 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 280
DB 890 TTGCTAGACACCAATATTCTCTGGGACAGTGTGTGGATCATGTTGGTGGAAATAATA 949
QY 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300
DB 950 AAGTCTCTAGAACACCAACAGAGGAGCAATATTAGAGAAATGAACCCCAATATACAGAA 1009
QY 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProAspThrPro 320
DB 1010 TTCAAAATCCCCCAATCAAGAGCACATCTCTGGACGAAGGTCTTTCCGCCGCCCACTCCA 1069
QY 321 ProGluAlaIleAlaLeuCysSerArgLeuGluTyrThrProThrAlaArgLeuThr 340
DB 1070 CCAGAGGCATTCGACATGTGTAGCCGTCTCTGGAGTACAGCCGACGCCGCCGCTAACCA 1129
QY 341 ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHis 360
DB 1130 CCACTGGAAGCTGTGCACATTCATTTTGTATGAATTCAGGACCCCAATGTCAAACTA 1189
QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
DB 1190 CCAATGGGCGAGACACACCTGCCCTCTTCAACTTTTACCACCTCAAGAACTGTCAAGTAAC 1249
QY 381 ProProLeuAlaThrIleLeuIleProProHisAlaArgIle 394
DB 1250 CCACCTCTGGCCACCATCTTATCCCTCTCACGCTCGGATT 1291

RESULT 5

US-09-216-958-2
; Sequence 2, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: Akhiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; DISEASES OF THE NERVOUS SYSTEM (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,

MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,958
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: rat
US-09-216-958-2
Alignment Scores:
Pred. No.: 3,82e-236 Length: 1972
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: 3 Gaps: 1
US-10-733-816-2 (1-394) x US-09-216-958-2 (1-1972)
QY 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
DB 110 GAAGGAAGAGTGAATCGAGAGAGCCATCATGTGGGGGCGACGAGAACACCTCTCTTT 169
QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
DB 170 GCGAGAGCTGCAAGCAGGTGCAGAGCCCTTACGCTTTGTAGCATGAAAGTTAGCAGA 229
QY 41 AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60
DB 230 GATAAAGATGGCAGCAAGGTAAACACAGTGTGGCAACTCTCTGACAGAGGTCTCTGACAGG 289
QY 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
DB 290 CCACAGAGTCAAGTTTACACAGACACTAAAGTCAATTGGAATGGGTCAATTGGTGTGTA 349
QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
DB 350 TATCAAGCCAACTTTGTGACTCAGGAGAACTGTGGCCCATCAAGAAAGTTCTTCAGGAC 409
QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
DB 410 AAGCGATTTAAGAACCCGAGAGCTCCAGATCATGAGAAAGTAGATCACTGTAACATAGTC 469
QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
DB 470 CGATTGGGTATTTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACCTTAACCTG 529
QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
DB 530 GTGCTGACTATGTTCCGGAACAGTGTACAGAGTCCGACAGACATATAGTCTGAGCCAG 589
QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180


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Db 1216 TTTGGAAGTCAAAGCAGCTGGTCCGAGGAGAACCCCAATGTTGGTATATCTGTTCTCGG 1275
Qy 231 TTTTyrArgAlaProGluLeuLeuPheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 1276 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTTAGTATAGATGA 1335
Qy 251 TTPSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 1336 TGGTCTGCTGCTGTGTGGCTGAGCTGTACTAGGACAAACCAATATTTCCAGGGGAT 1395
Qy 271 SerGlyValAspGlnLeuValGluIleIleIleValLeuGlyThrProThrArgGluGln 290
Db 1396 AGTGGTGTGATCAGTTGGTAGAAATAATCAAGTCTCTGGGAACCTCCAAAGGGAGCAA 1455
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 1456 ATCAGAGAAATGAACCCAACTACACAGATTTAAATTCCTCAATTAAGGCACATCCT 1515
Qy 311 TTPThrIleValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 1516 TGGACTAAGGTCTTCCGACCCGAACTCCACCGAGGCAATTGCACCTGTGTAGCCGCTG 1575
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1576 CTGGAGTATACACCAACTGCCCCGACTAACACCACTGGAAGCTTGTGCACATTCATTTT 1635
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1636 GATGAATTACGGGACCCCAATGTCCAACTACCAATGGGCGAGACACCTTGCACCTTC 1695
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
Db 1696 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCCTTATTCCTCT 1755
Qy 391 HisAlaArgIle 394
Db 1756 CATGCTCGGATT 1767

RESULT 7
US-08-461-018A-1
; Sequence 1, Application US/08461018A
; Patent No. 6071694
; GENERAL INFORMATION:
; APPLICANT: AKIHICO TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
```

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; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
; US-08-461-018A-1

Alignment Scores: 1.73e-235 Length: 2088
Pred. No.: 2010.00 Matches: 382
Score: 99.7% Conservative: 1
Percent Similarity: 99.7% Mismatches: 1
Best Local Similarity: 96.6% Indels: 0
Query Match: 3 Gaps: 0
DB:

US-10-733-816-2 (1-394) x US-08-461-018A-1 (1-2088)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 616 ATGTCAGGGCGGCCAGAACCCCTCTTTCCGAGAGCTGCAAGCCGGTGCAGACGCT 675
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 676 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACACAGGACGCGCAAGGTTGACACAGTG 735
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 736 GTGGCAACTCTCTGGGAGGGTCCAGACAGGCGCACAAAGAAAGTTCAGCTATACAGACACTAA 795
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 796 CTCATTGGAAATGGATCATTTGGTGGGTATATCAAGCCCAACTTTGTGATTGAGGAA 855
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 856 CTGGTCCCATCAAGAAAGTATTGCGAGGACAGAGATTTAAGAAATCGAGAGCTCCAGATC 915
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 916 ATCAGAAAGCTAGATCACGTAACTAGTCCGATTCGGTATTTCTTCTTACTCCAGTGT 975
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 976 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTCGGAACAGTATAC 1035
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 1036 AGAGTTGCGACACACTATAGTCAGGCCAACACAGACGCTCCCTGTGATTATGTCAGTTG 1095
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 1096 TATATGTATCAGCTGTTCCGAAGTTAGCTATATCATTTCTCTTGGAACTGCCATCGG 1155
Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 1156 GATATTAAACCCGAGAACTCTTTGTTGGATCTCTGATACCTGCTGTATTTAAACACTCTGTGAC 1215
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 1216 TTTGGAGGTGCAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTCGG 1275
Qy 231 TTTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 1276 TACTATAGGACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGA 1335
Qy 251 TTPSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
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Db 1336 TGGCTGCTGGCTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT 1395
Qy 271 SerGlyValAspGlnLeuValGluLeuIleLeysValLeuGlyThrProThrArgGluGln 290
Db 1396 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGGAGCAA 1455
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLeysPheProGlnIleLeysAlaHisPro 310
Db 1456 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAATTAAGGCACATCCT 1515
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCySerArgLeu 330
Db 1516 TGGACTAAGTCTTCCGACCCCGAATCTCCACGGAGGCAATTGCACCTGTAGCCGCTG 1575
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1576 CTGGAGTATACACCACTGCCCGACTAACCACTGGAAGCTTGTGCACATTTCATTTT 1635
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1636 GATGAATATAGGGGACCCAAATGTCAAACTACCAATGCGGAGACACACCTGCACCTTC 1695
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
Db 1696 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCT 1755
Qy 391 HisAlaArgIle 394
Db 1756 CATGCTCGGATT 1767

RESULT 8

US-09-216-958-1
; Sequence 1, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,958
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,018
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA

; ORIGINAL SOURCE:
; ORGANISM: human being
; US-09-216-958-1

Alignment Scores: 1.73e-235 Length: 2088
Pred. No.: 2010.00 Matches: 382
Score: 99.7% Conservativeness: 1
Percent Similarity: 99.7%
Best Local Similarity: 99.5%
Query Match: 96.6%
Indels: 0
Gaps: 0
DB: 3
US-10-733-816-2 (1-394) x US-09-216-958-1 (1-2088)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 616 ATGTCAGGGCGGCCAGAACCCCTCTCTTTGCGAGAGCTGCAAGCGGTGCAGACGCT 675
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 676 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGGACGCGCAGAGGTGACACAGTG 735
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 736 GTGGCAACTCTGGCGAGGGTCCAGACAGGCCACAAAGAGTCAGCTATACAGACACTAA 795
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 796 CTCATTGGAAATGGATCATTTGGTGGTATATATCAAGCCAACTTTGTGATTCCAGGAA 855
Qy 91 LeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 856 CTGGTCGCCATCAAGAAAGATTTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 915
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 916 ATCAGAAAGCTAGATCAGTAACTAGTCCGATTGCGTTATTTCTTACTCCAGTGT 975
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 976 GAGAAGAAAGATGAGTCTATCTTAATCTGGTCTGACTATCTTCGGGAAACAGTATAC 1035
Qy 151 AtgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 1036 AGAGTTGCCACACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTATATGTCAGTTG 1095
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyLysCysHisArg 190
Db 1096 TATATGTATCAGCTGTTCCGAAGTTTAGCTATATCATCTCTTGGAACTCCCATCGG 1155
Qy 191 AspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 1156 GATATTAAACCCGACGACCTCTTTGTTGGATCCTGTGATCTGTATATAAACTCTGTGAC 1215
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 1216 TTTGGAAAGTCAAGCAGCTGTCGAGGAGAACCAATGTTTCGTATATCTGTCTCGG 1275
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 1276 TACTATAGGGCACACAGATTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 1335
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 1336 TGGTCTGCTGGCTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT 1395
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 1396 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGGAGCAA 1455
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 1456 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAATTAAGGCACATCCT 1515

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QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 1516 TGGACTAAGGCTCTCCGACCCCGAACTCCACCGAGGCAATTCGACTGTGTAGCGCTG 1575
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1576 CTGGAGTATACCAACTGCCGACTAACCACTGGAAGCTTGTGACACATTCATTTTTT 1635
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1636 GATGAATTACGGGACCCCAATGTCAAACTACCAATGGGCGAGACACACCTGCACCTTC 1695
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
Db 1696 AACTTCACCACTCAAGAAGTGTCAAGTAATCCACTCTGGCTACCATCTTATTCCTCT 1755
QY 391 HisAlaArgIle 394
Db 1756 CATGCTCGGATT 1767

RESULT 9
US-09-566-921-24
; Sequence 24, Application US/09566921
; Patent No. 668288
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566, 921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 1952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 234735.15
US-09-566-921-24

Alignment Scores:
Pred. No.: 2,15e-186 Length: 1952
Score: 1609.00 Matches: 312
Percent Similarity: 86.8% Conservative: 24
Best Local Similarity: 80.6% Mismatches: 37
Query Match: 77.3% Indels: 14
DB: 3 Gaps: 3

US-10-733-816-2 (1-394) x US-09-566-921-24 (1-1952)
QY 8 GlyGlyCysMetSerGlyArgProArgThr---ThrSerPheAlaGluSerCysLysPro 26
Db 107 GCGCGAGGAGGAGCGAGGAGCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 157
QY 27 ValGlnGlnProSerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLys 46
Db 158 -----GGGGTGAAGCTGGGCGCT-----GACAGCGGGAAG 187
QY 47 ValThrThrValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyr 66
Db 188 GTGACCAAGTCTGTAGGCACTCTAGGCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 247
QY 67 ThrAspThrLysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCys 86
Db 248 ACGGACATCAAGTATGGCAATGGCTCATTTGGGCTCGTGTACAGGAGGAGGAGGAGGAGGAG 307
QY 87 AspSerGlyGluLeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArg 106
Db 308 GAGACCGGGAAGTAGTTCGCCCATCAAGAGGTTCTCCAGGACCAAGAGGTTCAAGAACCGGA 367
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QY 107 GluLeuGlnIleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePhe 126
Db 368 GAGCTCAGATCATGCGTAAGCTGGACCACTGCAATATTTGTGAGGCTGAGATACATTTTTC 427
QY 127 TyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPro 146
Db 428 TACTCCAGTGGCGAGGAAGAGAGAGAGCTTTACCTAAATCTGGTGTGGATATGTGCC 487
QY 147 GluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIle 166
Db 488 GAGACAGTGTACCGGCTGGCGCCCACTTCCACCAAGGCCAAGTTGACCATCCCTATCCTC 547
QY 167 TyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGly 186
Db 548 TATGTCAAGGTGTACATGTACCAAGCTCTTCCGAGCTTCTCCGAGCTTGGCTACATCCATCCCAAGGC 607
QY 187 IleCysHisArgAspIleLysProGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 206
Db 608 GTGTGTACCGGACATCAAGCCCAAGAACCTGTGTGTGAGCCCTGACACTGTGTGTCTC 667
QY 207 LysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyr 226
Db 668 AAGCTCTGCGATTTTGGCAGTGCAGAGCAGTTGGTCCGAGGGGAGGCCAATGTCTCTCTAC 727
QY 227 IleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSer 246
Db 728 ATCTGTCTCGCTACTACCGGCGCCAGAGCTCATCTTTGGAGCCACTGATTACACCTCA 787
QY 247 SerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlnProIle 266
Db 788 TCATCGATGTTTGGTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
QY 267 PheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrPro 286
Db 848 TTCCCTGGGAGCAGTGGGCTGGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
QY 287 ThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIle 306
Db 908 ACCCGGGAACAAATCCGAGAGATGAACCCCACTACACGAGGTTCAAGTTCCCTCAGATT 967
QY 307 LysAlaHisProTrpThrLysValPheArgProArgThrProGluAlaIleAlaLeu 326
Db 968 AAGCTCACCCCTGGGACAAAGGTGTTCAATCTCGAACCCGCGGAGGCCATCGGCTC 1027
QY 327 CysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAla 346
Db 1028 TGCTCTAGCTGTGTGAGTACACCCCATCTCTCAAGGCTCTCCCACTAGAGGCTGTGG 1087
QY 347 HisSerPheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThr 366
Db 1088 CACAGCTTCTTTGATGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
QY 367 ProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIle 386
Db 1148 CCCCTCTCTTCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
QY 387 LeuIleProProHisAlaArg 393
Db 1208 CTCATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1267

RESULT 10
US-09-488-856A-3
; Sequence 3, Application US/09488856A
; Patent No. 6316259
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP
; FILE REFERENCE: RPS-0115
; CURRENT APPLICATION NUMBER: US/09/488, 856A
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; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)...(1543)
US-09-488-856A-3

Alignment Scores:
Pred. No.: 2,546-186 Length: 2154
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 43
Best Local Similarity: 71.8% Mismatches: 44
Query Match: 77.3% Indels: 58
DB: Gaps: 4

US-10-733-816-2 (1-394) x US-09-488-856A-3 (1-2154)
Qy 5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
Db 107 CCTTCGGGAGCGCGCCCTGGGGCTCGGCAGCGCGGCTAGCTGTTTCGGCGAG--- 163
Qy 24 CysLysPro-----ValGlnGln 29
Db 164 -----CCCGCGCGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 217
Qy 30 ProSerAlaPheGlySerMetLys----- 37
Db 218 CCAGCGGCGACCGCGCGCGGAGGCGCATCTGTCTGGGGCCATGGTGGGGCGCTCGGGGCC 277
Qy 37 ----- 37
Db 278 TCGAGCTCCGGGGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 337
Qy 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 338 GGCACCTAGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 397
Qy 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrThr 69
Db 398 GTCTAGCCACTCTAGGCCAAGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 457
Qy 70 LysValIleGlyAenGlySerPheGlyValValThrGlnAlaLysLysLysAspSerGly 89
Db 458 AAGTGATTGGCAATGCTCATTTGGGGTCTGTGTACCGAGCAGCGCTGGCAGAGCAGG 517
Qy 90 GluLeuValAlaLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109
Db 518 GAACCTAGTCGCATCAAGAGGTTCTCCAGGACAAAGAGTTCAAGAACCGAGAGCTCAG 577
Qy 110 IleMetArgLysLysLysAspHicCysAsnIleValArgLeuArgTyrPheThrSerSer 129
Db 578 ATCATGCTAGCTGGACCACTGCATATTTGTAGGCTGAGATCTTTTCTACTCCAGT 637
Qy 130 GlyLysLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149
Db 638 GGCAGAGAAGAACGAGCTTTACTTAATCTGGTGTGGAATATGTGCCGAGACAGTG 697
Qy 150 TyrArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
Db 698 TACCGGGTGGCGCGCCACTTCCACAGCCCAAGTTGACCATCCCTATCTCTATGTCAAG 757
Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyLysCysHis 189
Db 758 GTGTACATGTACCAAGCTCTTCCGAGCTTGGCCCTACATCCATCCCGAGGGCGGTGTGCAC 817
Qy 190 ArgAspLysProGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 209
Db 818 CGCGACATCAAGCCCGAGAACCTGTGTGGAGCCCTGACACTGTGTCTCAAGCTCTGC 877

RESULT 11
US-09-578-194-6
; Sequence 6, Application US/09578194
; Patent No. 6822139
; GENERAL INFORMATION:
; APPLICANT: Sudwestdeutsche Saatzaucht-SWS
; APPLICANT: Advanta Seeds B.V.
; TITLE OF INVENTION: Modulation of Storage Organs
; FILE REFERENCE: 026-1
; CURRENT APPLICATION NUMBER: US/09/578,194
; CURRENT FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(1636)
; OTHER INFORMATION: strain Columbia ecotype
; OTHER INFORMATION: taxon:3702
; OTHER INFORMATION: tissue type leaves
; OTHER INFORMATION: clone lib lambda ZAPII
; PUBLICATION INFORMATION:
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lechamy, A. and Kreis, M.
; TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)
; TITLE: from Arabidopsis thaliana ( Accession No. 6822139 X94938, x94939 and X99696)
; TITLE: (008)
; JOURNAL: Plant Physiol.
; VOLUME: 113
; ISSUE: 1
; PAGES: 306-306
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; DATE: 1997-01-01
; DATABASE ACCESSION NUMBER: genbank/x94938
; DATABASE ENTRY DATE: 1998-02-13
; RELEVANT RESIDUES: (1) .. (1636)
US-09-578-194-6

Alignment Scores:
Pred. No.:      6,52e-142      Length:      1636
Score:          1245.00        Matches:      244
Percent Similarity: 75.1%      Conservative: 58
Best Local Similarity: 60.7%    Mismatches:  70
Query Match:    59.8%          Indels:       30
DB:             3              Gaps:         9

US-10-733-816-2 (1-394) x US-09-578-194-6 (1-1636)
QY 13 GlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnProSerAla 32
Db 63 GGGCTCTCTCAGCGCTCGGCTTTAGCTCCT-----CAGCGCGCGCATCTT 107
QY 33 PheGly-----SerMetLys-----ValSerArgAspLysAsp-----43
Db 108 CACGGCGGAGATTCTTTGAAACGTCGTCGCGATATAGACAAACGACAAAGGAAATGTCTGCT 167
QY 44 -----GlySerLysValThrThrValValAlaThr 53
Db 168 GCTGTTATAGAAAGAAATGATGCTGTATCCGGTCCACATAATTTCTACTACAATTGGA---224
QY 54 ProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLysValIleGly 73
Db 225 ---GGCAAAATGGTGAACCTAAACAGACCATTAAGTTTACATGCGCGAAGCGTTGTTGGA 281
QY 74 AsnGlySerPheGlyValValThrGlnAlaLysLeuCysAspSerGlyGluLeuValAla 93
Db 282 ACAGGATCATTCGGAATGTTATCCAGGCAAAATGCTTGGAACATCGAGAAATCAGTAGCC 341
QY 94 IleLysIysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMetArgLys 113
Db 342 ATTAAGAAGGTTTTGCAAGATCCCGTTATAAACCGAGAGTGCATTAATTAATGCGACTA 401
QY 114 LeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGlyGluLysLys 133
Db 402 ATGGACATCCAAATGGTTTCTTGAGCATGTGTTCTCTCTACA---ACGACTAGA 458
QY 134 AspGluValThrLeuAsnLeuValLeuAspTyrValProGluThrValTyrArgValAla 153
Db 459 GATGAGCTCTTCCTCAATCTCGTTATGAGTATGATGACGAGACATTCACCGGGTTTG 518
QY 154 ArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeuTyrMetTyr 173
Db 519 AAGCACTATAGTAGTTCAAAACCGCGATGCGCTATCTTCTATGTCAAACTTTACACATAC 578
QY 174 GlnLeuPheArgSerLeuAlaTyrIleHisSerPhe---GlyIleCysHisArgAspIle 192
Db 579 CAAATCTTCAGAGCGTTGGCTTATATCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
QY 193 LysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAspPheGly 212
Db 639 AAACCAACAAATCTTTTGGTTGATCCCAACCCATCCAGTGAAGCTCTGTGATTTTGA 698
QY 213 SerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArgTyrTyr 232
Db 699 AGTGCAAAAGTACTGTGTGAAGGTGAACCAACCAATATATATATATATATATATATATATAT 758
QY 233 ArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspValTrpSer 252
Db 759 CGAGCTCCAGAACTCATCTTTGTGTCACAGATATACATCCATTAATATATATATATATATAT 818
QY 253 AlaGlyCysValLeuAlaGluLeuLeuGlnGlyGlnProIlePheProGlyAspSerGly 272
Db 819 GCTGGTTGTGTTCTGCGAGAGTACTTCTTGGCAGCCGTTATTCGCGGAGAAATTTCT 878
QY 273 ValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGlnIleArg 292
Db 879 GTGGACCACTAGTGGAGATCATAAAGGTTCTTGGTACTCCAACCTCGCGAAGAAATCCGG 938
QY 293 GluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProTyrThr 312
Db 939 TGCATGAAACCAAACTACACAGACTTCAGATCCCAAAATCAAGCCCAACCTTGGCAT 998
QY 313 LysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLysLeuGlu 332
Db 999 AAGGTTTTCCAAAGCGGATGCTCGGGAAGCCATTCGACCTTCATCTCGGCTTCTTCA 1058
QY 333 TyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPheAspGlu 352
Db 1059 TACTACCAAGTCTACGTTGCACTGCGCTCGAGCATGTGCGCATCCGTTTTCATGAA 1118
QY 353 LeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheAsnPhe 372
Db 1119 CTCGGTGAGCAAAATGCTGCTTCCAAATGGCCGACCTCTACACCGTGTGTTCAACTTC 1178
QY 373 ThrThrGlnGluLeuSer---SerAsnProProLeuAlaThrIleLeuIleProProHis 391
Db 1179 ---AAACAAGAGTTGTCTGGGCTTCACCGGAGCTTATCAACAGGCTAATACCAAGCAT 1235
QY 392 AlaArg 393
Db 1236 GTGAGG 1241

RESULT 12
US-09-347-801-9
; Sequence 9, Application US/09347801
; Patent No. 6282345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
US-09-347-801-9

Alignment Scores:
Pred. No.:      8.94e-142      Length:      1814
Score:          1244.50        Matches:      246
Percent Similarity: 73.2%      Conservative: 54
Best Local Similarity: 60.0%    Mismatches:  90
Query Match:    59.8%          Indels:       20
DB:             3              Gaps:         5

US-10-733-816-2 (1-394) x US-09-347-801-9 (1-1814)
QY 3 TyrMetProMetGluGlyGlyMetSerGlyArg-ProArgThrThr-----18
Db 212 TATATAGCTCTTCGCGAGCATGCGCTCGGTGGCGGCGGCGCTCTCTTTGGGATTCA 271
QY 19 ----SerPheAlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLys 37
Db 272 GAATGGCAAGATTCCTAGCAGTCAGCCAGATCGTCTTCCCAACGAGTGTGGCAGTATGAG 331
QY 37 sValSerArgAspLysAspGlySerLysValThr-----49
Db 332 CATAGGAGCAGCAAGGACGTTGAAGATATTGTAGTCAATGTGGCAATGGCGGCGAGCGCTG 391
QY 50 -----ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyr 66
Db 392 TCATATCATAGTGACCAGCATTTGATGGAGAAATGGGCGGCAAGACGACCATTAGTTA 451
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QY 66 rThrAspThrLysValIleGlyAenGlySerPheGlyValValThrGlnAlaLysLeuCy 86
Db 452 CATGGCTGAGCGGTGTAGTGTATGGCTCTTCGGAACCGTTCCTCCAGGCCAAGTGCT 511
QY 86 sAspSerGlyGluLeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnAr 106
Db 512 TGAACCTGGTGAGACCGTGTATATAAAGGTTCTTCAAGACAAGAGATCAAGATCG 571
QY 106 gGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePh 126
Db 572 TGAGCTGCAAAACCATCGAGTGTTCACCAACCAAAATGTGTGCTCTAAAGCACTGTTT 631
QY 126 eTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPr 146
Db 632 CTTCTCAAAGACTGAG---AAAGAGGAGCTTTACCTCAATTTGGTGTCTGAGTATGACC 688
QY 146 oGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValI 166
Db 689 GGAGACTGCTCATCGTGTCTAAACATTAACAAGATGAACAGCGCATGCTTTGAT 748
QY 166 eTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHis---SerPh 185
Db 749 TTATGCAAAACTGTATATGATGATCAGATTGTGTAGAGCCTTGGCATACATTCAACAGCAT 808
QY 185 eGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaVa 205
Db 809 TGGAGTGTGCCACAGGACATTAAAGCGCAAAATCTCTGTTAATCTCTATCCCATCA 868
QY 205 lLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSe 225
Db 869 GCTAAATATTGTGACTTTGGCAGCGGAAAGTTCTGTGTAAAGGCGAACAATTC 928
QY 225 rTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrTh 245
Db 929 TTACATCTGTTCTAGGTACTACAGAGCTCCAGAGCTCATATTGGTGTCTACTGAATACAC 988
QY 245 rSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnPr 265
Db 989 AACAGCCATTGATGTTGGGTCTGTGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1048
QY 265 oIlePheProGlyAspSerGlyValAspGlnLeuValGluIleLysValLeuGlyTh 285
Db 1049 TCTGTTCCCTGGAGAAACCGGTGTGTATCAGCTTGTGTAATCATCAAGTCTTGGGCAC 1108
QY 285 rProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGl 305
Db 1109 ACCACACGTTGAAGAAATTAAGTGTATGAATCCAAATTTATACCGAGTTAAATTCGCGCA 1168
QY 305 nIleLysAlaHisProTrpThrLysValPheArgProArgThrProGluAlaIleAl 325
Db 1169 AATCAAAAGCTCACCATGGCATAGATATTTCCATAAAGAGATGCTGCTCAAGCGGTAGA 1228
QY 325 aLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCy 345
Db 1229 TCTGTTCCAGGCTTCTGAGTACTCACCAAACTTCAGTCTGCTGCTGCTGCTGCTGCTGCT 1288
QY 345 sAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAs 365
Db 1289 GGTCCATCCGTTCTTTCATGAACCTTCGGGATCCAAACACCGCTTACCGAATGGTCTGTT 1348
QY 365 pThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnPro---ProLeuAl 384
Db 1349 TCTTCCGCTCTCTCTCAATTTTAAAGCCCATAGAGCTGAAGAAGCTGCCGCGGATTTTCAT 1408
QY 384 aThrIleLeuIleProHisAlaArg 393
Db 1409 GGTGAATTTGGTCTCTGAGCATGACCG 1436
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RESULT 13

US-09-854-731-9

; Sequence 9, Application US/09854731

; Patent No. 6794561

GENERAL INFORMATION:

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; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-854-731-9
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Alignment Scores:

Pred. No.:	8 94e-142	Length:	1814
Score:	1244.50	Matches:	246
Percent Similarity:	73.2%	Conservative:	54
Best Local Similarity:	60.0%	Mismatches:	90
Query Match:	59.8%	Indels:	20
DB:	3	Gaps:	5

US-10-733-816-2 (1-394) x US-09-854-731-9 (1-1814)

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QY 3 TyrMetProMetGluGlyGlyMetSerGlyArg-ProArgThrThr----- 18
Db 212 TATATAGCTCTGTCCGAGCATGGCTCGGTGGCGTGGCAGCGCTCTCTTTGGGATTCA 271
QY 19 ----SerPheAlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLy 37
Db 272 GAATGCCACAAGTCTTAGCAGTGACCCAGATCGTCTCCCAACAGAGTGTGGCGATGAG 331
QY 37 sValSerArgAspLysAspGlySerLysValThr----- 49
Db 332 CATACGGGACGACAGGACGTTGAAGATATTGTAGTCAATGGCAATGGGCGGAGCTGG 391
QY 50 -----ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTy 66
Db 392 TCATATCATAGTGACCGCATTTGATGGAGAAATGGCGACGAAAGCAGACCATTAGTTA 451
QY 66 rThrAspThrLysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCy 86
Db 452 CATGGCTGAGCGGTGTGTAGTCTTCGGAAACCGTTCCTCCAGGCCAAGTGCT 511
QY 86 sAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnAr 106
Db 512 TGAACCTGGTGAGACCGTGTATATAAAGGTTCTTCAAGACAAGAGATCAAGAATCG 571
QY 106 gGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePh 126
Db 572 TGAGCTGCAAAACCATCGAGTGTTCACCAACCAAAATGTGTGCTCTAAAGCACTGTTT 631
QY 126 eTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValPr 146
Db 632 CTTCTCAAAGACTGAG---AAAGAGGAGCTTTACCTCAATTTGGTGTCTGAGTATGACC 688
QY 146 oGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValI 166
Db 689 GGAGACTGCTCATCGTGTCTAAACATTAACAAGATGAACAGCGCATGCTTTGAT 748
QY 166 eTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHis---SerPh 185
Db 749 TTATGCAAAACTGTATATGATGATCAGATTGTGTAGAGCCTTGGCATACATTCAACAGCAT 808
QY 185 eGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaVa 205
Db 809 TGGAGTGTGCCACAGGACATTAAAGCGCAAAATCTCTGTTAATCTCTATCCCATCA 868
QY 205 lLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSe 225
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Db      869  GCTAAATTTGTGACCTTTGGCAGCGCGAAAGTTCTCGTAAAGCGCAACCAACATTTTC 928
Qy      225  rTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrTh 245
Db      929  TTACATCTGTCTTAGGTACTACAGAGCTCCAGAGCTCATATTTGGTGTACTGAATACAC 988
Qy      245  rSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnPr 265
Db      989  AACAGCCATTGATGTTGGGTCTGCTGGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTG 1048
Qy      265  oIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysValLeuGlyTh 285
Db      1049  TCTGTTCCCTGGGAAGCGGTGTGTGATGAGTCTGTTGAATCATCAAGGTTCTGGGCAC 1108
Qy      285  rProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProG1 305
Db      1109  ACCCACAGCTGAAGAAATTAAGTGCATGAATCCAAATTATACCGAGTTTAAATTCGCCGA 1168
Qy      305  nIleLysAlaHisProThrLysValPheArgProArgThrProProGluAlaIleAl 325
Db      1169  AATCAAGACTCACCCATGGCATAAGATATTCCATAAAGAGATGCTGCTGAAGCGGTAGA 1228
Qy      325  aLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCy 345
Db      1229  TCTCGTCTCAGGCTTCTGAGTACTACCAACAACTTCGCTGCTGCTGCTGCTGCTGCTG 1288
Qy      345  sAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAs 365
Db      1289  GGTCCATCCGTTCTTTGATGAACCTTCGGGATCCAAACACCCGCTTACCGAATGGTCTTT 1348
Qy      365  pThrProAlaLeuPheAsnPheThrThrGlnGlnLeuSerSerAsnPro---ProLeuAl 384
Db      1349  TCTTCGCGCTCTCTTCAATTTTAAGCCCACTAGCTGAAGAACGTGCGCGCGATTTCAT 1408
Qy      384  aThrIleLeuIleProProHisAlaArg 393
Db      1409  GGTGAATTTGGTCCCTGAGCATGCACGG 1436
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RESULT 14

US-09-347-801-15
; Sequence 15, Application US/09347801
; Patent No. 6262345

GENERAL INFORMATION:

; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
US-09-347-801-15

Alignment Scores:

Pred. No.:	2,78e-141	Length:	1673
Score:	1240.00	Matches:	232
Percent Similarity:	78.6%	Conservative:	65
Best Local Similarity:	61.4%	Mismatches:	69
Query Match:	59.6%	Indels:	12
DB:	3	Gaps:	5

US-10-733-816-2 (1-394) x US-09-347-801-15 (1-1673)

Qy 21 AlaGluSerCysLysProValGlnGln-----ProSerAlaPheGlySerMet 36

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Db      101  GCAGTCGCCCTCGCAGAGAAGCAGCAGATGGCGAGCGCGTATGCGAGGGGAAACAC 160
Qy      37  LysValSerArgAspLysAspGlySerLysValThrThrValValAlaThrProGlyGln 56
Db      161  GCCATGACC-----GGTCACATCATCTCCACCAACCATCGGC-----GGCAAG 202
Qy      57  GlyProAspArgProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySer 76
Db      203  AACGGCGAGCCCAAGCAGCAGATTAGCTACATGCGGAGCGCGTTGTGGCCTGTTTCG 262
Qy      77  PheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLys 96
Db      263  TTTGGCATCTCTTTTCAAGCTAAATGCTGCGAAACCGGAGAGATGGTGGGCATTAAAG 322
Qy      97  ValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHis 116
Db      323  GTACTGCAGCAGCAGCGGTACAGACCGTGTGAGCTGCAGCTTATCGCTTCGATGATCAT 382
Qy      117  CysAsnIleValArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluVal 136
Db      383  TCCAATGTTTCTCCCTCAAGCAGCTGCTTCTTCTCAACC---ACAGTAGAGATGAGCTG 439
Qy      137  TyrLeuAsnLeuValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyr 156
Db      440  TTCTTGAACTTGTATGGAGTATGTCGCGAGACGCTATACCGCGTGTCTTAAGCAGCTAC 499
Qy      157  SerArgAlaLysGlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPhe 176
Db      500  AGTAATGCCAACCAACGAGGATGCCGCTTATCTATGTCAAGCTTTACATGATCAGCTTTT 559
Qy      177  ArgSerLeuAlaTyrIleHisSerPhe---GlyIleCysHisArgAspIleLysProGln 195
Db      560  AGAGGGCTAGCTTATGTTCATCTGTTTCCAGGAGTTTGGCCACAGGAGTGTGAACACAA 619
Qy      196  AsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLys 215
Db      620  AATGTTTGTGTTGATCTCTTAACCCATCAAGTCAAGATCTGTGACTTTTGAAGTGCANAA 679
Qy      216  GlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaPro 235
Db      680  GTTCTGTGCTGCTGGTGAACCAACATAGCATATATGCTCTCGCTACTATCGTGTCTCT 739
Qy      236  GluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCys 255
Db      740  GAGCTCATATTTGGTGCACCTGAATATACAACTTCAATAGACATATGCTCAGCTGGATGT 799
Qy      256  ValLeuAlaGluLeuLeuGlnProIlePheProGlyAspSerGlyValAspGln 275
Db      800  GTTCTTTGCAGAGCTACTTCTTGTGTCAGCTCTGTTTCCAGGAGAGACTGCGGTGTGATCAG 859
Qy      276  LeuValGluIleLysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsn 295
Db      860  CTAGTGGAGATTATCAAGGTTCTTGGTACTTCCAAACCGTGAAGAAATTCGGTGCATGAAC 919
Qy      296  ProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProThrThrLysValPhe 315
Db      920  CCCAACTATACCGAGTTTCAGGTTTCTCAGATTAAAGGCTCATCTCTGGCACAAGATTTTC 979
Qy      316  ArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrPro 335
Db      980  CACAAGAGAAATGCCCGCTGAAGCTATAGATCTTGGCTCCCGCTCTCTCCAGTATTACCA 1039
Qy      336  ThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAsp 355
Db      1040  AATCTAGTTGCACTGCTCTTGTATGATGTGACATCTCTTCTTGTATGACTACGTGAG 1099
Qy      356  ProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGln 375
Db      1100  CCGAATGCAGCTTGGCGAATGGCCGCCATTCCTCTCTGTTCAACTTCAAACCTGAA 1159
Qy      376  GluLeuSerSerSerAsnProProLeuAlaThrIleLeuIleProProHisAlaArg 393
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: September 18, 2006, 01:33:44 ; Search time 1472 Seconds
(without alignments)
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Title: US-10-733-816-2
Perfect score: 2081
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA.Main -OFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPT=0 -UNITS=bits -START=1 -END=1
-MATRIX=BLOSUM62 -TRANS=human04.cdi -LIST=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes05p
-USER=US10733816 @CGN 1.1.2530 @runat 15092006_085455_15819 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LOGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
1	2024	97.3	1389	7	US-10-181-543-3	Sequence 3, Appli

2	2024	97.3	1389	7	US-10-305-720-1414	Sequence 1414, Ap	
3	2024	97.3	1389	9	US-10-772-636-71	Sequence 71, Appl	
4	2024	97.3	1389	10	US-10-840-060-256	Sequence 256, Appl	
5	2024	97.3	1389	16	US-11-288-493-71	Sequence 71, Appl	
6	2015	96.8	1525	16	US-11-004-762-15	Sequence 15, Appl	
7	2015	96.8	1972	3	US-09-866-712-2	Sequence 2, Appli	
8	2013	96.7	1231	10	US-10-504-173-44	Sequence 44, Appl	
9	2013	96.7	1263	9	US-10-482-524-6	Sequence 6, Appli	
10	2013	96.7	1389	9	US-10-482-524-3	Sequence 3, Appli	
11	2013	96.7	1815	9	US-10-357-930-30285	Sequence 30285, A	
12	2012	96.7	1474	16	US-11-004-762-17	Sequence 17, Appl	
13	2010	96.6	1503	7	US-10-613-728-7	Sequence 7, Appli	
14	2010	96.6	2088	3	US-09-866-712-1	Sequence 1, Appli	
15	1996.5	95.9	1639	8	US-10-278-759-13	Sequence 13, Appl	
16	1996.5	95.9	1639	8	US-10-302-812-61	Sequence 61, Appl	
17	1996.5	95.9	1639	9	US-10-828-669-10	Sequence 10, Appl	
18	1996.5	95.9	1639	10	US-10-887-553A-275	Sequence 275, App	
19	1996.5	95.9	1639	10	US-10-770-726-21	Sequence 21, Appl	
20	1925	92.5	1665	16	US-11-136-527-3081	Sequence 3081, Ap	
21	1750.5	84.1	1864	7	US-10-062-674-1877	Sequence 1877, Ap	
22	1634.5	78.5	1698	10	US-10-491-467-65	Sequence 65, Appl	
23	1609	77.3	1452	9	US-10-482-524-5	Sequence 5, Appli	
24	1609	77.3	1952	10	US-10-765-700-24	Sequence 24, Appl	
25	1609	77.3	2154	7	US-10-181-875-3	Sequence 3, Appli	
26	1609	77.3	2169	6	US-10-278-759-11	Sequence 11, Appl	
27	1609	77.3	2169	9	US-10-482-524-1	Sequence 1, Appli	
28	1609	77.3	2169	10	US-10-887-553A-274	Sequence 274, App	
29	1609	77.3	2170	6	US-10-278-759-9	Sequence 9, Appli	
30	1609	77.3	2374	9	US-10-723-860-4597	Sequence 4597, App	
31	1607	77.2	2155	10	US-10-486-706-241	Sequence 241, App	
32	1607	77.2	2167	16	US-11-136-527-2430	Sequence 2430, Ap	
33	1542.5	74.1	3477	10	US-10-840-060-254	Sequence 254, App	
34	1542.5	74.1	3477	13	US-11-097-143-4571	Sequence 4571, Ap	
35	1294	62.2	1849	7	US-10-292-408-2	Sequence 2, Appli	
36	1273	61.2	1922	8	US-10-437-963-29872	Sequence 29872, A	
37	1262	60.6	2164	8	US-10-424-599-133605	Sequence 133605, A	
38	1259.5	60.5	1523	7	US-10-292-408-23	Sequence 23, Appl	
39	1258.5	60.4	1639	8	US-10-425-114-36269	Sequence 36269, A	
40	1257.5	60.4	1813	8	US-10-425-114-31098	Sequence 31098, A	
C	41	1257.5	60.4	1831	8	US-10-437-963-98579	Sequence 98579, A
42	1257.5	60.4	1881	8	US-10-425-114-32039	Sequence 32039, A	
43	1257.5	60.4	1980	9	US-10-425-115-49442	Sequence 49442, A	
44	1254.5	60.3	2794	8	US-10-437-963-9996	Sequence 9996, Ap	
45	1252	60.2	1675	8	US-10-425-114-30667	Sequence 30667, A	

ALIGNMENTS

RESULT 1
US-10-181-543-3
; Sequence 3, Application US/10181543
; Publication No. US20030211608A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; APPLICANT: Jacquelline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION
; FILE REFERENCE: RTSP-0339
; CURRENT APPLICATION NUMBER: US/10/181,543
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-10-181-543-3

Alignment Scores:
Pred. No.: 1,16e-240 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 7 Gaps: 0

US-10-733-816-2 (1-394) x US-10-181-543-3 (1-1389)

Qy 11 MetSerGlyArgProGlnGlyProValGlnGlnPro 30
Db 40 ATGTGAGGGCGCCAGAACCTCTTTGGGAGAGCTGCAAGCGGTGCAGAGCCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGGACGCGCAGCAACAGTG 159
Qy 51 ValAlaThrProGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGCCACAGAACTCAGCTATACAGACTAAA 219
Qy 71 ValileGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCyAspSerGlyGlu 90
Db 220 GTGATTGGAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTGAGGAA 279
Qy 91 LeuValAlaLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAGATTGTCAGACAGAGATTTAAGAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCATCTGAATAGTCCGATGCGTTGATTCTTCTACTCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAGAAGATGAGGTCTATCTTAATCTGTGCTGGACTATGTTCCGGAAACAGTATAC 459
Qy 151 ArgValAlaAlaHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
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Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGTATCAGCTGTTCCGAAGTTTAGCCCTATATCCATTTCTTTGGAAATCTGCCATCGG 579
Qy 191 AspLysLysProGlnAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLysLeuCyAsp 210
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Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
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Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 700 TACTATAGGACCAGAGTTGATCTTTGGAGCCACTGATTATATACCTCTAGTATAGATGTA 759
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTGCTGCTGTGTGTGGCTGAGCTGTACTAGCAACCAATATTTTCCAGGGAT 819
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 820 AGTGGTGTGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAAGGGAGCAA 879
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
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Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCySerSerArgLeu 330

940 TGGACTAAGGTCTTCCGACCCCGAACTCCACCGGAGGCAATTCACCTGTGTAGCGGTCTG 999
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Db 1000 CTGGAGTATACACAACTGCCGACTAACACCACTGGAAGCTTGTGCACATTCATTTTT 1059
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
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Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
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Qy 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191

RESULT 2
US-10-305-720-1414
; Sequence 1414, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1414
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank ID No. US20040010136A1 5529236
US-10-305-720-1414

Alignment Scores:
Pred. No.: 1,16e-240 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 7 Gaps: 0

US-10-733-816-2 (1-394) x US-10-305-720-1414 (1-1389)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTGAGGGCGCCAGAACCTCTTTGGGAGAGCTGCAAGCGGTGCAGAGCCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGGACGCGCAGCAACAGTG 159
Qy 51 ValAlaThrProGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGCCACAGAACTCAGCTATACAGACTAAA 219
Qy 71 ValileGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCyAspSerGlyGlu 90
Db 220 GTGATTGGAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTGAGGAA 279
Qy 91 LeuValAlaLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAGATTGTCAGACAGAGATTTAAGAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
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Db 400 GAGAAGAAGATGAGGTCTATCTTAATCTGTGCTGGACTATGTTCCGGAAACAGTATAC 459
Qy 151 ArgValAlaAlaHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
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Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
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Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
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Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
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Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTGCTGCTGTGTGTGGCTGAGCTGTACTAGCAACCAATATTTTCCAGGGAT 819
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
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Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 880 ATCAGAGAAATGAACCCAAACTACACAGAAATTTAAATTTCCCTCAAAATTAAGAGCATCTCT 939
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Db 340 ATGAGAAAGCTAGTCACTGTAACATAGTCGGATTGGTTATTTCTTCTACTCCAGTGGT 399
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Db 400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGluThrLeuProValIleTyrValLysLeu 170
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Db 460 AGAGTTGGCCAGACACTATATGTCAGCCAAACAGACGCTCCCTGTGATTTATGTCAGATTG 519
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
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Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
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Db 580 GATATTAAACCGCAGAACCTCTTGTGGATCCTGATACCTGCTGTATTAATAAACTCTGTAC 639
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
    |||||
Db 640 TTTGGAAGTCAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTGTCTCGG 699
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
    |||||
Db 700 TACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATATATACCTCTAGTATAGATGA 759
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
    |||||
Db 760 TGGTCTGCTGCTGTGTGGTGGCTGAGCTGTACTAGCAACAACCAATATTTCCAGGGGAT 819
Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
    |||||
Db 820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGTCTCTGGAACTCCAAACAAGGGAGCAA 879
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
    |||||
Db 880 ATCAGAGAATGAAACCAACTACACGAAATTTAATTCCTCANATTAGGCACATCCT 939
Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
    |||||
Db 940 TGGACTAAGGTCTTCGACCCCGAACTCCACCGGAGCAATTCACCTGTGTAGCCGCTG 999
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
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Db 1000 CTGGAGTATACACCAACTGCCCGCACTAACCACTGGAAGCTGTGACACATTCATTTT 1059
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyValArgAspThrProAlaLeuPhe 370
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Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
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Qy 391 HisAlaArgIle 394
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RESULT 3
US-10-772-636-71
; Sequence 71, Application US/10772636
; Publication No. US20050042687A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
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; TITLE OF INVENTION: 5014
; FILE REFERENCE: MP103-01SPIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/772,636
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-10-772-636-71
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Alignment Scores:
Pred. No.: 1.16e-240 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 9 Gaps: 0
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US-10-733-816-2 (1-394) x US-10-772-636-71 (1-1389)

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Qy 11 MetSerGlyValArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTCAAGGGCGGCCCAAGACCACCTCTTTCCGAGAGCTGCAGCGGTGCAGCAGCCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGAGACAAGCAGCGCAGCAAGGTGACAACAGTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAGACTGAGCTATATACAGACACTAAA 219
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTGAGAGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAAGTATTTCAGGACAAGAGATTTAAGAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCAGTCACTGTAACATAGTCCGATTCGGTTATTTCTTACTCCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGAGCTATGTTCCGGAACAGTATAC 459
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Db 820 AGTGGTGGATCAGTTGGTAGAAATAATCAAGTCTCGGAACCTCCAAACAGGAGCAA 879
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 880 ATCAGAGAAATGAACCAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 939
Qy 311 TTPThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 940 TGGACTAAGGCTCTCCGACCCCACTCCACCGGAGCAATTGCACCTGTGTAGCCGCTG 999
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1000 CTGGAGTATACACCACTGCCGCACTAACCACTGGAAGCTGTGACATTCATTTT 1059
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1060 GATGAATACGGACCCCAATGTCAAAATCCAAATCGGCGAGACACACCTGCACCTTTC 1119
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCCTTATTCCTCT 1179
Qy 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191

RESULT 5
US-11-288-493-71
; Sequence 71. Application US/11288493
; Publication No. US20060078947A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; FILE REFERENCE: MP103-015PIRNONMIN
; CURRENT APPLICATION NUMBER: US/11/288,493
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US/10/772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
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FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-11-288-493-71
Alignment Scores:
Pred. No.: 1,16e-240 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 16 Gaps: 0

US-10-733-816-2 (1-394) x US-11-288-493-71 (1-1389)
Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 40 ATGTCAGGGGGGGCCCAAGACCACTCCTTTTCGAGAGAGCTGCAAGCCGGTGACAGCGCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGCAAGGACGCGCAGCAAGGTGACAACTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCGGCGAGGTCAGACAGGCCCAAGAGTCAGCTATACAGACACTAAA 219
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATGGATCAITTTGTGTGTATATCAAGCCAAACTTGTGTATTCAGGAGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAAGTATTTCAGGACACAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCACTGTAACATAGTCGAGTTCGATTTCTTCTACTCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAGAAAGATCAGGCTATCTTAATCTGTGCTGGACTACTGTTCGGGAACAGTATAC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACTATAGTCAGGCAACACAGACGCTCCCTGTGATTATGTCAAGTTG 519
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGTATCAGCTGTTCGGAAGTTTAGCCTATATCCATTCCTTTGGAAATCTGCCATCGG 579
Qy 191 AspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGCAGAACCTCTTTGTTGGATCCTGTGATCTGCTATTAAAACCTCTGTGAC 639
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 640 TTTTGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCAAATGTTTCGTATATCTGTCTCTCGG 699
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 700 TACTATAGGCGCACAGAGTTGATCTTTTGGAGCCACCTGATTATATACCTCTAGTATAGATGTA 759
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTGTGGCTGTGTGTGGCTGTAGCTGTACTAGGACCAACCAATATTTTCCAGGGGAT 819
Qy 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
Db 820 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCCTGGGAACCTCCAAACAGGAGCAA 879
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
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Db 880 ATCAGAGAATGAACCAACTACAGAAATTTAAATTCCTCAATTAAGGCACATCCT 939
 QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
 Db 940 TGGACTAAGGTCTTCGACCCGAACTCCACCGAGGCAATTCGCACTGTGTAGCCGCTG 999
 QY 331 LeuGluThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
 Db 1000 CTGGAGTATACACAACTGCCCGCACTAACCACTTGAAGCTTGTGCACATTCATTTTT 1059
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
 Db 1060 GATGAATTACGGGACCCCAATGTCAACATCCAAATGGGCGAGACACACCTGCACCTTC 1119
 QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
 Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCCTCT 1179
 QY 391 HisAlaArgIle 394
 Db 1180 CATGCTCGGATT 1191

RESULT 6

US-11-004-762-15
 ; Sequence 15: Application US/11004762
 ; Publication No. US20060003953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Madeline M. Butler
 ; APPLICANT: Nicholas M. Dean
 ; APPLICANT: Kenneth W. Dobie
 ; APPLICANT: Joshua Finger
 ; APPLICANT: Ravi Jain
 ; APPLICANT: Robert McKay
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Kathleen Myers
 ; TITLE OF INVENTION: Compositions and their uses directed to bone growth modulators
 ; FILE REFERENCE: BIOLO050US
 ; CURRENT APPLICATION NUMBER: US/11/004,762
 ; CURRENT FILING DATE: 2004-12-03
 ; PRIOR APPLICATION NUMBER: US 60/527,370
 ; PRIOR FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/527,173
 ; PRIOR FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/527,172
 ; PRIOR FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/527,420
 ; PRIOR FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/527,174
 ; PRIOR FILING DATE: 2003-12-04
 ; PRIOR APPLICATION NUMBER: US 60/527,397
 ; PRIOR FILING DATE: 2003-12-04
 ; NUMBER OF SEQ ID NOS: 680
 ; SOFTWARE: PatentSeq version 1.0
 ; SEQ ID NO 15
 ; LENGTH: 1525
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-004-762-15

Alignment Scores:
 Pred. No.: 1,79e-239 Length: 1525
 Score: 2015.00 Matches: 386
 Percent Similarity: 98.0% Conservative: 0
 Best Local Similarity: 98.0% Mismatches: 2
 Query Match: 96.8% Indels: 6
 DB: 16 Gaps: 1

US-10-733-816-2 (1-394) x US-11-004-762-15 (1-1525)

QY 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
 Db 110 GAAGGAAAGGTGAATCGAGAGAGCCATCATGTGCGGGCGACCGAGAACCACTCCTCTTT 169

QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
 Db 170 GCGGAGAGCTGCAGCCAGCTGCAGCAGCCTTCAGCTTTTGGTAGCATGAAGATTAGCAGA 229
 QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
 Db 230 GATTAAGATGGCAGCAGGTTAACCAAGTGGTGGCACTCCTGGACAGGGTCTCTGACAGG 289
 QY 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
 Db 290 CCACAGGAAGTCAAGTTACACAGACACTAAAGTCATTGGAAATCGGTCACTTTGGTGTGTA 349
 QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
 Db 350 TATCAAGCCAAACTTTGTGACTCAGAGAACTGGTGGCCATCAAGAAAGTTCTTCAGGAC 409
 QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
 Db 410 AAGCGATTTAAGAACCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTC 469
 QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
 Db 470 CGATTGCGGTATTCTTCTACTCGAGTGGCGAGAGAAAGATCAGGTCTACCTTAACCTG 529
 QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
 Db 530 GTGCTGGACTATGTTCCGAAACAGTGTACAGAGTCGCCAGACACTATAGTCAGGCCAAG 589
 QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
 Db 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTACCAGCTGTTCAGAACTTAGCC 649
 QY 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
 Db 650 TATATCACTTCCTTTGGGACTCGCCATCGAGACATTAACCAACAGAACCTCTTGCTGGAT 709
 QY 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
 Db 710 CTTGATACAGCTGTATTAACACTCTCGACTTTGGAAGTGCAGAGCTGGTGGCCGAGGA 769
 QY 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
 Db 770 GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCACCCAGAGCTGATCTTTGA 829
 QY 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
 Db 830 GCCACCGATTACACAGTCTAGTATAGATGTATGCTCGAGGCTGTGTGTTGGCTGAATTG 889
 QY 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle 280
 Db 890 TTGCTAGGACAACCAATATTTCTGGGGACAGTGGTGGTGGATCAGTTGGTGGAAATATA 949
 QY 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300
 Db 950 AAGTCTCTAGGAACACCAACAGGGAGCAAAATTAGAGAAATGAACCAAAATTATACAGAA 1009
 QY 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320
 Db 1010 TTCAAATTCGCCCAATCAAGGCACATCTCTGGACGAAGGCTCTTCGGCCGCCCAACTCCA 1069
 QY 321 ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340
 Db 1070 CCAGAGGCAATCGACATGTGTACCGCTCTCCTCGAGTACACGCCGACCCGCCGCTAACCA 1129
 QY 341 ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360
 Db 1130 CCACTGGAAGCTTGTGCACATTCATTTTTTGTGAATTACGGGACCCCAAAATGTCAAACTA 1189
 QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
 Db 1190 CCAATGGGGCGAGACACCTGCCCTCTTCACTTTTACCCTCAAGAACTGTCAAGTAAC 1249

QY 381 ProProLeuAlaThrIleLeuLeuLeuProProHisAlaArgIle 394
Db 1250 CCACCTCTGGCCACCATCTTATCTCCCTCCTCAGCTCGGATT 1291

RESULT 7
US-09-866-712-2
; Sequence 2, Application US/09866712
; Patent No. US20020058637A1
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY
; INHIBITING NEURONAL CELL DEATH AND TREATING ALZHEIMER'S DIS
; KINASE I (AS AMENDED)

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROOTH, LIND & PONACK
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/866,712
FILING DATE: 30-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/216,958
FILING DATE: December 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2001-0488/LC/00177

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)721-8200
TELEFAX: (202)721-8250
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1972 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: rat
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-866-712-2

Alignment Scores:
Pred. No.: 2,71e-239 Length: 1972
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: 3 Gaps: 1

US-10-733-816-2 (1-394) x US-09-866-712-2 (1-1972)

QY 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
Db 110 GAAGGAAAGGTGATCGAAGAGGCCATCATGTGGGGGCGCCGAGAACCACTCTTT 169

QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40
Db 170 GCGGAGAGCTGCAAGCCAGTGCAGCAGCTTTCAGCTTTTGGTAGCATGAAAGTTAGCAG 229

QY 41 AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60
Db 110 GCGGAGAGCTGCAAGCCAGTGCAGCAGCTTTCAGCTTTTGGTAGCATGAAAGTTAGCAG 229

Db 230 GATAAAGATGGCAGCAGGTAAACACAGCTGGTGGCAACTCTCTGGACAGGGTCTCTGACAGG 289
QY 61 ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
Db 290 CCACAGGAGTCAAGTTACACAGACACTAAAGTCAATTGGAATGGGTCAATTGGTGTGGTA 349

QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGluAsp 100
Db 350 TATCAAGCCAAACTTTGTGACTCAGGAGAACTGGTGGCCATCAAGAAAGTTCTTTCAGGAC 409

QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
Db 410 AAGCGATTAAAGAACCCAGAGCTCCAGATCATGGAAGAGCTAGATCACTGTACATAGTC 469

QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
Db 470 CGATTGCGGTATTCTTCTACTCGAGTGGCGAGAGAAAGATGAGGTCTACTCTTAACCTG 529

QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLys 160
Db 530 GTGCTGGACTATGTTCGGAAACAGTGTACAGAGTCGCCAGACACTATATGTTCGAGCCAA 589

QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
Db 590 CAGACACTCCCTGTGATCTATGTCAGTTGTATATGTACAGCTGTTTCAGAGTCTAGCC 649

QY 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
Db 650 TATATCCATTCTTGGGATCTGCCATCGAGACATTAACACACAGAACCTCTTGTCTGGAT 709

QY 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
Db 710 CCTGATACAGCTGTATTAAACTCTGCGACTTTGGAGAGTCAAAGCAGCTGGTCCGAGGA 769

QY 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
Db 770 GAGCCCAATGTTTCATATATCTGTTCTCGTACTACAGGCGCACAGAGCTGAATTTGGA 829

QY 241 AlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
Db 830 GCCACCGATTACACGCTTAGTATAGATGTATGTCTGCGGTCAGGCTGTGTGGCTGAATTG 889

QY 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle 280
Db 890 TTGCTAGGACCAACCAATATTCTCTGGGACAGTGGTGTGGATCAGTTGGTGGAAATATA 949

QY 281 LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu 300
Db 950 AAGTCTCTAGGAACACCAACAGGGAGCAATTTAGAGAAATGAACCCCAATTTATACAGAA 1009

QY 301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320
Db 1010 TTCAAAATTCGCCCAATCAAGGCACATCTTTGGACGAAGGTCTTTGGCCCCGCAACTCCA 1069

QY 321 ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340
Db 1070 CCAGAGGCAATCGCACTGTGTAGCCGCTCTCTCGAGTACACGCGGACCGCCGCTTAACA 1129

QY 341 ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360
Db 1130 CCACTGGAGCTTGTGCACATTTATTTTTTGTGAATATACGGAGCCCAATGTCAACTA 1189

QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
Db 1190 CCAATGGGGGAGACACACCTGCCCTCTTCAACTTTTACCCTCAAGAACTGTCAAGTAAC 1249

QY 381 ProProLeuAlaThrIleLeuIleProProHisAlaArgIle 394
Db 1250 CCACCTCTGGCCACCATCTTATCTCCCTCCTCAGCTCGGATT 1291

RESULT 8

US-10-504-173-44

; Sequence 44, Application US/10504173

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; Publication No. US20050202428A1
; GENERAL INFORMATION:
; APPLICANT: Axordia Limited
; TITLE OF INVENTION: Pluripotential Stem Cells
; FILE REFERENCE: P101863WO
; CURRENT APPLICATION NUMBER: US/10/504,173
; CURRENT FILING DATE: 2004-08-11
; PRIOR APPLICATION NUMBER: 0203359.5
; PRIOR FILING DATE: 2002-02-02
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-504-173-44

Alignment Scores:
Pred. No.: 2,25e-239 Length: 1231
Score: 2013.00 Matches: 383
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 96.7% Indels: 0
DB: 10 Gaps: 0

US-10-733-816-2 (1-394) x US-10-504-173-44 (1-1231)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
DB 37 ATGTCAGGGCGGCCAGAACCACTCTCTTTGCGAGAGCTGCAAGCGGTGCAGAGCCT 96
QY 31 SerAlaPheGlySerMetIysValSerArgAspIysAspGlySerIysValThrVal 50
DB 97 TCAGCTTTTGGCAGCATGAAGATTAGCAGAGCAAGACGCGCAGCAAGGTGCAACAGTG 156
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
DB 157 GTGGCACTCTCTGGCAGGTTCAGACAGCCACAGAGATTAAGAAATCGAGAGCTCAATA 216
QY 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
DB 217 GTGATTGGAATGGATCATTTGGTGGTATATCAAGCCAAACTTTGTGATTCAGAGAA 276
QY 91 LeuValAlaIleLysIysValLeuGlnAspIysArgPheLysAsnArgGluLeuGlnIle 110
DB 277 CTGGTCGCCATCAAGAAGATTATTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 336
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
DB 337 ATGAGAAAGCTAGATCACTGTAACATAGTCGATTGGTATTCTTCTACTCCAGTGT 396
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
DB 397 GAGAAGAAGATGAGGTCTATCTTAATCTGTGCTGGACTATGTTCCGGAACAGTATAC 456
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGluThrLeuProValIleTyrValLysLeu 170
DB 457 AGAGTTGCCAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTTATGCAAGTTG 516
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 517 TATATGATCAGCTGTTCGAGTTAGCCCTATATCAATCTCTTGGAACTGCCATCG 576
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
DB 577 GATATTAACCCGAGAACCTCTTTGGTGGATCCTGATCTGCTGTATTAAACACTCTGTGAC 636
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
DB 637 TTTGGAAGTCAAGACGCTGGTCCGAGGAAACCCCAATGTTTGTATATCTGTTCTCGG 696
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
; TACTATAGGGCACCAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 756
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuLeuGlyGlnProIlePheProGlyAsp 270
DB 757 TGGTCTGCTGGCTGTGTGGCTGAGCTGTTACTAGGACACCAATATTTCCAGGGGAT 816
QY 271 SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln 290
DB 817 AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTGGGAACTCAACAGGGAGCAA 876
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
DB 877 ATCAGAGAATGAACCCAACTACACAGAAATTAATTCCTCAATTAAGGCACATCCT 936
QY 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuLeuCysSerArgLeu 330
DB 937 TGGACTAAGGTCTTCCGACCCCACTCCACCGAGGCAATTGCACTGTGTAGCCGTCTG 996
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
DB 997 CTGGAGTATACACCAACTGCCGACTAACACCACTGGAAGCTTGTGCACATTCATTTT 1056
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
DB 1057 GATGAATTAAGGGACCCCAATGTCAAACTACCAATGGGCGAGACACACCTGCACCTTC 1116
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
DB 1117 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGTACCACCTTATTTCTCCT 1176
QY 391 HisAlaArgIle 394
DB 1177 CATGCTCGGATT 1188

RESULT 9
US-10-482-524-6
; Sequence 6, Application US/10482524
; Publication No. US20040261137A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham PLC
; APPLICANT: Holder, Julie C
; TITLE OF INVENTION: Models for Metabolic Disorders
; FILE REFERENCE: PG4458
; CURRENT APPLICATION NUMBER: US/10/482,524
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB 0115570.4
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: GB 0205604.2
; PRIOR FILING DATE: 2002-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Coding nucleic
; OTHER INFORMATION: acid sequence of the transgene used for the
; OTHER INFORMATION: production of GSK-3 beta transgenic non-human
; OTHER INFORMATION: animals
US-10-482-524-6

Alignment Scores:
Pred. No.: 2,35e-239 Length: 1263
Score: 2013.00 Matches: 383
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 96.7% Indels: 0
DB: 9 Gaps: 0

US-10-733-816-2 (1-394) x US-10-482-524-6 (1-1263)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
```

Db 1 ATGTGAGGGCGGCCAGAACCTCTCTTTCGGAGAGCTGCAAGCGGTGCAGCAGCCT 60
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 61 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGAGCGCAGCAAGGTGACACAGTG 120
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70
Db 121 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCGCAAGAGTGCAGCTATACAGACATAA 180
QY 71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 181 GTGATTGGAAATGGATCATTTGTGTGTATATCAAGCCAACTTTGTGATTCAGAGAA 240
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 241 CTGGTCGCCATCAAGAAAGATTATTCAGGACAGAGATTTAAGAAATCGAGAGCTCCAGATC 300
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 301 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTTATTCTTCTACTCCAGTGT 360
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 361 GAGAAAGATGAGGTCTATCTTAACTCTGTGCTGACTATGTTCCGAAACAGTATAC 420
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 421 AGAGTTGCCAGACACTATAGTCAGGCCAACACAGCGCTCCCTGTGATTATGTCAAGTTG 480
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 481 TATATGTATCAGCTGTTCGAACTTAGCCCTATATCCATTCCTTTGGAATCTGCCATCGG 540
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 541 GATATTAAACCGCAGAACCTCTTGTGGATCCTGTACTGCTGTATTAACAACTCTGTGAC 600
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 601 TTTGGAGTGCAGAGCAGCTGGTCCAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG 660
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 661 TACTATAGGCGCACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 720
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 721 TGTCTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGCAACCAATATTTCCAGGGGAT 780
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 781 AGTGGTGTGGATCAGTTGGTAGAAATATCAAGTCTCTGGAACTCCACAGGGAGCAA 840
QY 291 IleArgGluMetAsnProHentTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 841 ATCAGAGAAATGAACCAACTACAGAAATTTAAATTCCTCAAATTAAGGCACATCCT 900
QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 901 TGSACTTAAGGTCTTCCGACCCCGAACTCCACCGAGGCAATTGCACCTGTGTAGCCGCTG 960
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 961 CTGGAGTATACCAACTGCCCCGACTAACACCACTGGAGCTTGTGCACATTCATTTTTT 1020
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1021 GATGAATTACGGGACCCAAATGTCAAACCTACCAAAATGGGCGAGACACACCTGCACCTTC 1080
QY 371 AsnPheThrThrGlnLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390

Db 1081 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGCTGCTACCATCTTATTCCTCCT 1140
QY 391 HisAlaArgile 394
Db 1141 CATGCTCGGATT 1152
RESULT 10
US-10-482-524-3
; Sequence 3, Application US/10482524
; Publication No. US20040261137A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham PLC
; APPLICANT: Holder, Julie C
; TITLE OF INVENTION: Models for Metabolic Disorders
; FILE REFERENCE: PG4458
; CURRENT APPLICATION NUMBER: US/10/482,524
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB 0115570.4
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: GB 0205604.2
; PRIOR FILING DATE: 2002-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-524-3
Alignment Scores:
Pred. No.: 2,73e-239 Length: 1389
Score: 2013.00 Matches: 383
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 96.7% Indels: 0
DB: 9 Gaps: 0
US-10-733-816-2 (1-394) x US-10-482-524-3 (1-1389)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnPro 30
Db 40 ATGTCAAGGCGGCCAGACCACTCTCTTTCGGAGAGCTGCAAGCGGTGCAGCAGCCT 99
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAAGTTAGCAGACAGAGCGCAGCAAGGTGACACAGTG 159
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCGCAAGAGTTCAGCTATACAGACATAA 219
QY 71 ValileGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATGGATCATTTGTGTGTATATCAAGCCAACTTTGTGATTCAGAGAA 279
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAAGATTATTCAGGACAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTTATTCTTCTACTCCAGTGT 399
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAAAGATGAGGTCTATCTTAACTCTGTGCTGAGCTATGTTCCGAAACAGTATAC 459
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190

1045	TGGTCTCCTGGCTGTGTGTGGCTGAGCTGTTACTAGGACCAACAATATTTCCAGGGGAT	1104
Qy		
271	SerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrProThrArgGluGln	230
Db		
1105	AGTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGGAATCTCCAAACAGGGAGCAA	1164
Qy		
291	IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro	310
Db		
1165	ATCAGAGAAATGAACCCAAACTACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT	1224
Qy		
311	TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu	330
Db		
1225	TGGACTAAGGTCTTCCAGACCCGNACTCCACGGAGGCAATTGCACGTGTGTAGCCGCTCG	1284
Qy		
331	LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe	350
Db		
1285	CTGGAGTATACACCAACTGCCCGCACTAACACCACTGGGAAGCTTGTGCACATTCATTTTTT	1344
Qy		
351	AspGluLeuArgAspProAsnValIleHisProAsnGlyArgAspThrProAlaLeuPhe	370
Db		
1345	GATGAATTCGGGACCCAAATGTCAAATCTACAAATGGGGGAGACACCTGCACACTTC	1404
Qy		
371	AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro	390
Db		
1405	AAC TTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGGTACCACTCCTTATTCCTCCT	1464
Qy		
391	HisAlaArgIle	394
Db		
1465	CATGCTCGGATT	1476

RESULT 12

US-11-004-762-17
; Sequence 17, Application US/11004762
; Publication No. US2006003953A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Madeline M. Butler
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Joshua Finger
; APPLICANT: Ravi Jain
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Kathleen Myers
; TITLE OF INVENTION: Compositions and their uses directed to bone growth modulators
; FILE REFERENCE: BIOL00500S
; CURRENT APPLICATION NUMBER: US/11/004,762

Alignment Scores:	
Pred. No.:	4, 01e-239
Score:	2012.00
Percent Similarity:	98.0%
Best Local Similarity:	97.7%
Mismatches:	2
Conservative:	1
Matches:	385
Length:	1474

Query Match:	96.7%	Indels:	6
DB:	16	Gaps:	1
US-10-733-816-2 (1-394) x US-11-004-762-17 (1-1474)			
Qy	7	GlucylGlyGly:-----MetSerGlyArgProArgThrThrSerPhe	20
Db	85	GAAGAAAGAGTGAATCGAGAGAGCCATCATGTGGGGCCACCGAAGACCACTCCTTT	144
Qy	21	AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg	40
Db	145	GCGGAGAGCTGCAAGCCAGTCGAGCAGCTTCAGCTTTTGGTAGCATGAAGTTAGCAGA	204
Qy	41	AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg	60
Db	205	GATAAAGATGGCAGCAAGGTAAACACAGTGTGTGGCAACTCCTCGACAGGGTCTCGACAGG	264
Qy	61	ProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal	80
Db	265	CCACAGGAGTCAAGTACACAGACATTAAGTCAATGGAAATGGGTCAATTTGGTGTGTA	324
Qy	81	TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp	100
Db	325	TATCAAGCCAAACTTTGTGACTCAGAGAACTGGTGGCCATCAAGAAGTTCTTCAGGAC	384
Qy	101	LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal	120
Db	385	AAGCGATTTTAAGAACCGAGAGCTCCAGATCATCAGAAAGCTAGATCACTGTAACATAGTC	444
Qy	121	ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu	140
Db	445	CGATTCGGGTATTTCTTACTCTGAGTGGCAGAGAAAGATGAGGTCTACTTAACTTG	504
Qy	141	ValLeuAspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLys	160
Db	505	GTGCTGGACTATGTTCCGAAACAGTGTACAGAGTCGCCACAGACATATAGTCAGAGCAAG	564
Qy	161	GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla	180
Db	565	CAGACACTCCCTGTGATCTATGTCAAAGTTGTATATGTATACAGCTGTTTCAGAACTAGCC	624
Qy	181	TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuLeuAsp	200
Db	625	TATATCCATTCCTTTGGGATCTGCCATCGAGACATTAACACACAGAACTCTTGTCTGGAT	684
Qy	201	ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly	220
Db	685	CCTGATACAGCTGTATTAACACTCTGCACTTTGGAAAGTGCAAGACAGCTGGTCCGAGGA	744
Qy	221	GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly	240
Db	745	GAGCCCAATGTTTCATATATCTGTCTCGGTACTACAGGGCACAGAGCTGATCTTTGGA	804
Qy	241	AlaThrAspTyrThrSerSerIleAspValTyrPheSerAlaGlyCysValLeuAlaGluLeu	260
Db	805	GCCACCGATTACAGCTCTAGTATAGATATGTGTCTCGAGCTGTGTGTGGCTGAATTG	864
Qy	261	LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle	280
Db	865	TTGTAGGACAACCAATATTTCTTGGGGACAGTGTGTGTGATCAGTTGGTGGAAATAA	924
Qy	281	LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu	300
Db	925	ARGTCTCTAGGACACCCAAACAGGGAGCAATTAGAGAAATGAACCCAAATTATACAGAA	984
Qy	301	PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro	320
Db	985	TTCAATTTCCCAATCAAGGCACATCTCTTGACGAGAGGTCTTTCGGCCCCGAACTCCA	1044
Qy	321	ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr	340
Db	1045	CCAGAGCAATCGACTGTGTAGCCGTCTCTGGAGTACACGGCGGACCGCCGGCTAACCA	1104

QY 341 ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHis 360
DB 1105 CCACTGGAAGCTTGTGCACATTCATTTTGTGAAATACGGAGCCCAATATGCAAACTA 1164
QY 361 ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
DB 1165 CCAATGGGGGAGACACACCTGCGCTCTTCAACTTTTACCACCTCAAGAAGCTGTCAAGTAAC 1224
QY 381 ProProLeuAlaThrLeuLeuLeuProProHisAlaArgile 394
DB 1225 CCACCCCTGGCCACCATCTTATCCCTCTCAGCTCGGATT 1266
RESULT 13
US-10-613-728-7
; Sequence 7, Application US/10613728
; Publication No. US20040010813A1
; GENERAL INFORMATION:
; APPLICANT: Cincinnati Children's Hospital Medical Center
; APPLICANT: Robbins, Jeffrey
; TITLE OF INVENTION: A ROBUST, INDUCIBLE CARDIAC PREFERRED
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR TRANSGENESIS
; FILE REFERENCE: CHM02 G0053
; CURRENT APPLICATION NUMBER: US/10/613,728
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/393,525
; PRIOR FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(1295)
; OTHER INFORMATION: GSK-CA
US-10-613-728-7
Alignment Scores:
Pred. No.: 7,34e-239 Length: 1503
Score: 2010.00 Matches: 382
Percent Similarity: 99.7% Conservative: 1
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 96.6% Indels: 0
DB: 7 Gaps: 0
US-10-733-816-2 (1-394) x US-10-613-728-7 (1-1503)
QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
DB 33 ATGTGGGGGCGACCGAAGAACCGCGTTTTCGGAGAGCTGCAAGCCAGTGCAGAGCCT 92
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
DB 93 TCAGCTTTTGTAGTAGTAAGTTAGCAGAGATAAAGATGCGCAGCAAGGTAACACACAGTA 152
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnValSerThrAspThrLys 70
DB 153 GTGGCAACTCTCGCCAGGCTCTGACAGCCACAGGAAGTCAGTTATACAGACACGAAA 212
QY 71 ValileGlyAsnGlySerPheGlyValValThrGlnAlaLysLeuCysAspSerGlyGlu 90
DB 213 GTGATTGGAAATGATCATTTGTGTGTATATCAAGCCAACTTGTGATTCTGGAGAA 272
QY 91 LeuValAlaLeuLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
DB 273 CTGTTGGCCATCAAGAAAGTTCTACAGCAAGCGATTTAAGAACCGAGAGCTCCAGATC 332
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgThrPhePheThrSerSerGly 130
DB 333 ATGAGAAAGCTAGACCACTGATACATAGTCGAGCTCGGATTATTTCTTACTCGAGTGGT 392
QY 131 GluLysLysAspGluValThrLeuAsnValLeuValLeuAspThrValProGluThrValThr 150

DB 393 GAGAAGAAAGATGAGGTCTACCTTAACCTGGTCTGAGCATATGTTCCGGAGACAGTGTAC 452
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValLysValLysLeu 170
DB 453 AGAGTCGCCAGACACTATAGTCAGCAAGCAGACACTCCCTGTGATCTATGTCAAGTTG 512
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 513 TATATGTATCAGCTGTTCAGAGTCTAGCCCTATATCCATTCCTTTGGAAATCTGCCATCGA 572
QY 191 AspIleLysProGlnAsnLeuLeuLeuAspThrAlaValLeuLysLeuCysAsp 210
DB 573 GACATTAAACCAACAGAACCTCTTGTGGATCCTGTATACAGCTGTATTAATAACTCTGTGAC 632
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
DB 633 TTTTGAAGTGTCAAGCAGCTGTGTCGAGGAGAGCCCAATGTTTCATATATCTGTCTTCGG 692
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
DB 693 TACTACAGGCACACAGAGTTGATCTTTGGAGCCACTGATTACAGCTCCAGTATAGATGTA 752
QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyValLeuGlyThrProThrArgGluGln 270
DB 753 TGCTCTGCAGGCTGTGTGTGGCTGAATTGTTCTAGGACCAACCAATATTTCTCGGGAC 812
QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
DB 813 AGTGGTGTGATCAGTTGGTGGAAATAATAAAGGTCTTAGGAACACCAACAGGGAGCAA 872
QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
DB 873 ATTAGAGAAATGAACCCCAATATACAGAAATTCCTTCAATCAAGGACATCTCT 932
QY 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu 330
DB 933 TGGACAAAGGTCTTCCGGCCCCGAACTCCACACAGAGGCAATTGCACCTGTGCAGCCGTCTG 992
QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
DB 993 CTGGAGTACACACTACCGCCCGCTTAACACCACTGGAAGCTTGTGCACATTCATTTTTC 1052
QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyValArgAspThrProAlaLeuPhe 370
DB 1053 GATGAATTGGGGACCCCAATGTCAAACTTACCAATATGGGCGAGACACACCTGACTCTTC 1112
QY 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
DB 1113 AACTTTTACCACCTCAAGAACTGTCAAGTAACCCCCCTCTGGCCACCACCTCTTATCCCTCCA 1172
QY 391 HisAlaArgile 394
DB 1173 CATGCTCGGATT 1184
RESULT 14
US-09-866-712-1
; Sequence 1, Application US/09866712
; Patent No. US20020058637A1
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: METHODS OF INHIBITING TAU-PROTEIN KINASE I ACTIVITY
; INHIBITING NEURONAL CELL DEATH AND TREATING ALZHEIMER'S DISEASE
; KINASE I (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICANT: US/09/866,712
FILING DATE: 30-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/216,958
FILING DATE: December 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2001-0488/LC/00177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: nucleic acid
STRADEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: human being
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-866-712-1

Alignment Scores:
Pred. No.: 1,25e-238 Length: 2088
Score: 2010.00 Matches: 382
Percent Similarity: 99.7% Conservative: 1
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 96.6% Indels: 0
DB: 3 Gaps: 0

US-10-733-816-2 (1-394) x US-09-866-712-1 (1-2088)

QY	11	MetSerGlyArgProGlnThrThrSerPheAlaGluSerCysLysProValGlnGlnPro	30
DB	616	ATGTCAGGGCGGCCAGAACCTCTCTTGGGAGAGCTGCAAGCGCGGCGAGCGCT	675
QY	31	SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal	50
DB	676	TCAGCTTTTGGCAGCATGAAGTTAGCAGAGACAAAGGACGCGCAGGAGTGAACAGTG	735
QY	51	ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThrLys	70
DB	736	GTGGCAACTCTGGCGAGGGTCCAGACAGGCCCAAGAGTACGCTATACAGACACTAA	795
QY	71	ValIleGlyAsnGlySerPheGlyValValThrGlnAlaLysLeuCysAspSerGlyGlu	90
DB	796	CTCATTTGGAATGATGATTTGGTGGTATATCAAGCCAACTTTGTGATTCAGAGAA	855
QY	91	LeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle	110
DB	856	CTGGTCGCATCAAGAAGTATTGCGAGCAAGAGATTGAAGATCGAGAGCTCCAGATC	915
QY	111	MetArgLysLeuAspHisCysAniIleValArgLeuArgThrPhePheThrSerGly	130
DB	916	ATGAGAAAGCTAGATCACTCACTAATAGTCCGATGGTATTCTTCTACTCCAGTGT	975
QY	131	GluLysLysAspGluValThrLeuAsnLeuValLeuAspThrValProGluThrValThr	150
DB	976	GAGAGAAAGATGAGTCTATCTTAATCTGGTCTCGACTATGTTCCGGAACAGTATAC	1035
QY	151	AtqValAlaArgHisThrSerArgAlaLysGlnThrLeuProValIleThrValLysLeu	170
DB	1036	AGAGTTGCCAGACACTATAGTCAGCCAAACAGACCGCTCCCTGTGATTATGTAAGTTG	1095

QY	171	TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg	190
DB	1096	TATATGATATCAGCTGTTCCGAAGTTTAGGCTATATCCATTCTCTTGGAAATCTCCCATCGG	1155
QY	191	AspIleLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp	210
DB	1156	GATATTAAACCCGAGAACCTCTTGTGGATCCTGATACCTGCTGTTATTAACACTCTGTGAC	1215
QY	211	PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerThrIleCysSerArg	230
DB	1216	TTTGGAAAGTCAAAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCGG	1275
QY	231	TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal	250
DB	1276	TACTATAGGCACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGA	1335
QY	251	TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp	270
DB	1336	TGGTCTGCTGGCTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTTCCAGGGGAT	1395
QY	271	SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln	290
DB	1396	AGTGTGTGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGGAGCAA	1455
QY	291	IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro	310
DB	1456	ATCAGAGAAATGAACCCNAACTACACAGAAATTTAAATTCCTCAAAATTAAGGACACCTCT	1515
QY	311	TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu	330
DB	1516	TGGACTAAGTCTTCCGACCCGAACTCCACGGAGGCAATTCGACTGTGTAGCCGCTCTG	1575
QY	331	LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe	350
DB	1576	CTGGAGTATACACCAACTGCGGACTTAACACCACTGGAAGCTGTGCACATTCATTTT	1635
QY	351	AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe	370
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QY	371	AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro	390
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QY	391	HisAlaArgIle 394	
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; Sequence 13, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237.70020.US
; CURRENT APPLICATION NUMBER: US/10/278,759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-759-13

Alignment Scores: 4.06e-237 Length: 1639
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Score:

Percent Similarity: 96.5% Conservative: 0
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DB: 6 Gaps: 1

US-10-733-816-2 (1-394) x US-10-278-759-13 (1-1639)

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QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
DB 413 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCCAGGAA 472
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
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QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
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GenCore version 5.1.9
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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3	1996.5	95.9	1639	US-11-283-329-215
4	1974	94.9	1319	US-11-299-324-2
5	1961.5	94.3	1388	US-11-299-324-1
6	1919	92.2	1164	US-11-299-324-6
7	1808	86.9	1167	US-11-299-324-4

8	1609	77.3	2134	8	US-11-266-748A-347876	Sequence 347876, A
9	1609	77.3	2134	8	US-11-266-748A-381459	Sequence 381459, A
10	1609	77.3	2134	8	US-11-266-748A-431255	Sequence 431255, A
11	1609	77.3	2154	8	US-11-266-748A-28735	Sequence 28735, A
12	1609	77.3	2169	6	US-10-553-520-84	Sequence 84, Appl
13	1609	77.3	2200	8	US-11-266-748A-56261	Sequence 56261, A
14	1590.5	76.4	1545	6	US-10-795-135-4	Sequence 4, Appl
15	1416	68.0	837	8	US-11-299-324-13	Sequence 13, Appl
16	1355	65.1	950	8	US-11-266-748A-262739	Sequence 262739, A
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27	1278	61.4	2055	6	US-10-449-902-23629	Sequence 23629, A
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29	1263.5	60.7	1981	6	US-10-449-902-19717	Sequence 19717, A
30	1258	60.5	2082	9	US-11-056-355B-46578	Sequence 46578, A
31	1257.5	60.4	1969	9	US-11-218-305-17779	Sequence 17779, A
32	1257	60.4	1654	6	US-10-953-349-33012	Sequence 33012, A
33	1257	60.4	1654	9	US-11-056-355B-13202	Sequence 13202, A
34	1256	60.4	1715	9	US-11-056-355B-4901	Sequence 4901, Ap
35	1254.5	60.3	2624	6	US-10-449-902-24300	Sequence 24300, A
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38	1252	60.2	1795	9	US-11-056-355B-12500	Sequence 12500, A
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41	1247	59.9	1650	9	US-11-056-355B-43958	Sequence 43958, A
42	1246	59.9	1230	7	US-11-299-286-2358	Sequence 2358, Ap
43	1246	59.9	1634	9	US-11-056-355B-77777	Sequence 77777, A
44	1246	59.9	1718	9	US-11-056-355B-30399	Sequence 30399, A
45	1246	59.9	1718	9	US-11-056-355B-33989	Sequence 33989, A

ALIGNMENTS

RESULT 1
US-11-299-324-9
; Sequence 9, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-299-324-9

Alignment Scores:			
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DB:	8	Gaps:	0

US-10-733-816-2 (1-394) x US-11-299-324-9 (1-1263)

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RESULT 2
US-11-299-324-3
; Sequence 3, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; PRIOR FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-299-324-3
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Score: 1996.50 Matches: 383
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Query Match: 95.9% Indels: 13
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US-10-733-816-2 (1-394) x US-11-299-324-3 (1-1302)
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 ; Publication No. US20060127388A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cain, Michael
 ; APPLICANT: Yaworsky, Paul J
 ; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
 ; FILE REFERENCE: WYE-052
 ; CURRENT APPLICATION NUMBER: US/11/299,324
 ; CURRENT FILING DATE: 2005-12-09
 ; PRIOR APPLICATION NUMBER: US 60/634,813
 ; PRIOR FILING DATE: 2004-12-10
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 2
 ; LENGTH: 1319
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-299-324-2

Alignment Scores:
 Pred. No.: 6,23e-211 Length: 1319
 Score: 1974.00 Matches: 382
 Percent Similarity: 94.8% Conservative: 0
 Best Local Similarity: 94.8% Mismatches: 2
 Query Match: 94.9% Indels: 20
 DB: Gaps: 1

US-10-733-816-2 (1-394) x US-11-299-324-2 (1-1319)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
 Db 1 ATGTCAGGGCGGCCAGAACCACTCTCTTTCGGAGAGCTGCAAGCGCGTGCAGCAGCCT 60
 Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
 Db 61 TCAGCTTTTCGCAGCATGAAGTTAGCAGACAGCAAGACGCGCAGCAAGGTGCAACAGTG 120
 Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
 Db 121 GTGGCAACTCTCTGGCAGGGTCCAGACAGGCCCAAGAACTGAGTATACAGACACTAAA 180
 Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
 Db 181 GTGATGGAAATGGATCATTTGGTGGTATATCAAGCCCAAACTTTGTGATTCCAGAGAA 240
 Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
 Db 241 CTGGTCGCCATCAAGAAGATTTTCAGGACAAGAGATTTAAGAAATCAGAGCTCCAGATC 300
 Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
 Db 301 ATGAGAAGCTAGATCATCTGTAACATAGTCGGATTGGTTATTTCTTCTACTCCAGTGGT 360
 Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
 Db 361 GAGAAGAAGATGAGGTCTATCTTAATCTGTGTGCTGAGCTATGTTCCGGAAACAGTATAC 420

151 ArgValAlaAraGHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
 Db 421 AGAGTTTGCAGACACTATAGTCAGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 480
 Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 Db 481 TATATGTATCAGCTGTTCGGAAGTTAGCTATATCCATTCCTTTTGAATCTGCCATCG 540
 Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
 Db 541 GATATTAAACCCGAGAACCTCTTGTGGATCTCTGATCTGCTGATGTTATTAACACTCTGTGAC 600
 Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 Db 601 TTTGGAAGTGCRAAGCAGCTGTTCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCG 660
 Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
 Db 661 TACTATAGGGCACCAGAGTTGATCTTTTGGAGCCACTGATTATACCTCTAGTATAGATGA 720
 Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 Db 721 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTTACTAGGACAACCAATATTTCCAGGGGAT 780
 Qy 271 SerGlyValAspGlnLeuValGluIleIleLysVal----- 282
 Db 781 AGTGGTGTGGATCAGTTGGTAGAAATTAATCAAGGT-GTCCCCCAGAAATTCATATAAGC 839
 Qy 283 -----LeuGlyThrProThrArgGluGlnIle 291
 Db 840 AATCTAGGAAGTTTTCGACCTGGAAAGCTGCTCTGGAACTCCCAACAGGAGCAAAATC 899
 Qy 292 ArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProTyr 311
 Db 900 AGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCCATTAAGGCACATCCTCTGG 959
 Qy 312 ThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgGluLeu 331
 Db 960 ACTAAGGTCTTTCGACCCCGAACTCCACCGAGGCAATTCGACTGTGTAGCCCTGTGCTG 1019
 Qy 332 GluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPheAsp 351
 Db 1020 GAGTATACACCAACTGCCCCGACTAACACCACTGGAAGCTTGTGCACATTCATTTTGTAT 1079
 Qy 352 GluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheAsn 371
 Db 1080 GAATTCAGGGACCCAAATGTCAAACTACCAAAATGGCGGAGACACACCTGCACCTTTCAAC 1139
 Qy 372 PheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProProHis 391
 Db 1140 TTCACCACTCAAGAACTGTCAAGTAATCACCTCTGGCTACCATCTTATTCCTCTCAT 1199
 Qy 392 AlaArgile 394
 Db 1200 GCTCGGATT 1208

RESULT 5

US-11-299-324-1
 ; Sequence 1, Application US/11299324
 ; Publication No. US20060127388A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cain, Michael
 ; APPLICANT: Yaworsky, Paul J
 ; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
 ; FILE REFERENCE: WYE-052
 ; CURRENT APPLICATION NUMBER: US/11/299,324
 ; CURRENT FILING DATE: 2005-12-09
 ; PRIOR APPLICATION NUMBER: US 60/634,813
 ; PRIOR FILING DATE: 2004-12-10
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1
 ; LENGTH: 1388

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-299-324-1

Alignment Scores:
Pred. No.: 1,69e-209 Length: 1388
Score: 1961.50 Matches: 382
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 2
Query Match: 94.3% Indels: 43
DB: 8 Gaps: 1

US-10-733-816-2 (1-394) x US-11-299-324-1 (1-1388)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
DB 1 ATGTCAGGGCGGCCAGAACCACTCTTTGGGAGAGCTGCAAGCGGTGCAGAGCCT 60
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
DB 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGGACGCGCAAGGTGACACAGTG 120
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
DB 121 GTGGCAACTCTCTGGCAGGTCAGACAGGCCACAGAGATCTAGCTATACAGACATAA 180
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
DB 181 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGAGAA 240
QY 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
DB 241 CTGGTCGCCATCAAGAAAGATTATTCAGGACACAGAGATTTAAGAAATCGAGAGCTCCAGATC 300
QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
DB 301 ATGAGAAAGTACATCACTGTAACATAGTCCGATTCGGATTTCCTTACTCCAGTGT 360
QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
DB 361 GAGAAGAAAGATGAGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATAC 420
QY 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
DB 421 AGAGTTGCCACACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480
QY 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
DB 481 TATATGTATCAGCTGTTCGAAAGTTTAGCCCTATATCCATTCCTTTGGAATCTGCCATCGG 540
QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
DB 541 GATATTAAACCGCAGAACCTCTTTGGTGGATCCTGATCTGCTGATTAATAAATCTCTGAC 600
QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
DB 601 TTTGGAAGTGCAAAGCAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTCTTCTCGG 660
QY 231 TyrTyrArgAlaProGluLeuIlePheGlyValThrAspTyrThrSerSerIle----- 248
DB 661 TACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTAT-AGGTCA 719
QY 248 ----- 248
DB 720 ATAAAAAGTAGTCACCTGGACACAGATTTCACGCTCTCTTTGATAGTACATCTCACCACA 779
QY 248 ----- 248
DB 780 TCAGACCTTTAAAAATTTTGTGTGTCAACCATTTACTGTTCCTTCTTCTCTCTCCGTACT 839
QY 249 AspValTyrSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePhePro 268
DB 840 GATGTATGTCTGCTGGCTGTGTGTGGCTGTAGCTGTACTAGGACAAACCAATATTTCGA 899

; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-299-324-6

Alignment Scores:
Pred. No.: 7,51e-205 Length: 1164
Score: 1919.00 Matches: 364
Percent Similarity: 99.5% Conservative: 3
Best Local Similarity: 98.6% Mismatches: 2
Query Match: 92.2% Indels: 0
DB: 8 Gaps: 0

US-10-733-816-2 (1-394) x US-11-299-324-6 (1-1164)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
DB 1 ATGTCAGGGCGGCCAGAACCACTCTTTGGGAGAGCTGCAAGCGGTGCAGAGCCT 60
QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
DB 61 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAGGACGCGCAAGGTGACACAGTG 120
QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
DB 121 GTGGCAACTCTCTGGCAGGTCAGACAGGCCACAGAGATCTAGCTATACAGACATAA 180
QY 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
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Db 181 GTGATTTGGAAATGATCATTTGGTGGTATATCAAGCCAACTTTGTGATTCAGAGAA 240
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 241 CTGGTCCCATCAAGAAGATTATTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 300
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 301 ATGAGAAAGCTAGATCACTGATTAACATAGTCCGATTCGGTATTATTTCTACTCCAGTGGT 360
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 361 GAGAAAGAGATGAGTCTATCTATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 421 AGAGTTGCCAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 481 TATATGTATCAGCTGTTCGAAAGTTTAGCCTATATCCATTCCTTGGAAATCTGCCATCGG 540
Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 541 GATATTAAACCCGAGAACCTCTTTGTTGGATCCTGATACCTGCTGTATTAACACTCTGTGAC 600
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 601 TTTGGAAGTCAAAAGCAGCTGGTCCGAGGAGAACCCAAATGTTTCGTATATCTGTTCTCGG 660
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 661 TACTATAGGGCACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGA 720
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 721 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
Db 781 AGTGGTGTGATCAGTTGGTAGAAATAATCAAGTCTCGGAACTCCCAACAGGGAGCAA 840
Qy 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
Db 841 ATCAGAGAAATGAACCCAAACTACACAGAAATTTAAATTCCTCAAAATTAAGGCACATCCT 900
Qy 311 TrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu 330
Db 901 TGGACTAAGTCTTCCGACCCCGAACTCCACCGAGGCAATTCGACTGTGTAGCCGCTG 960
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 961 CTGGAGTATACACCAACTGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Qy 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db 1021 GATGAATTTAGGGACCCCAAAATGTCAAACTCAAAATGGCGGAGACACACCTGCACCTTC 1080
Qy 371 AsnPheThrThrGlnGluLeuSerSer 379
Db 1081 AACTTCACCACTCAAGATGCTAATACT 1107
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RESULT 7

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US-11-299-324-4
; Sequence 4, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
```

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; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-299-324-4

Alignment Scores:
Pred. No.: 2,07e-192 Length: 1167
Score: 1808.00 Matches: 351
Percent Similarity: 91.4% Conservatives: 0
Best Local Similarity: 91.4% Mismatches: 1
Query Match: 86.9% Indels: 32
DB: 8 Gaps: 1
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US-10-733-816-2 (1-394) x US-11-299-324-4 (1-1167)

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Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 1 ATGTCAGGGCGGCCCAAGAACCACTCTTTGGGAGAGCTGCAAGCCGGTGCAGCAGCCT 60
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 61 TCAGCTTTTGGCAGCATGAAGATTAGCAGACAAAGCAGCGCAGCAAGGTGACAAAGTG 120
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 121 GTGGCAACTCTCTGGGCGAGGGTCCAGACAGCCACCAAGAGTCAGCTATACAGACACTAA 180
Qy 71 ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 181 GTGATTTGGAATATGATCATTTGGTGGTATATCAAGCCAACTTTGTGATTCAGAGAA 240
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110
Db 241 CTGGTCCCATCAAGAAGATTATTCAGGACCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 300
Qy 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 301 ATGAGAAAGCTAGATCACTGTAACATAGTCCGATTCGGTATTATTTCTACTCCAGTGGT 360
Qy 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
Db 361 GAGAAAGAGATGAGGCTCTATCTTAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 421 AGAGTTGCCAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTG 480
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 481 TATATGTATCAGCTGTTCGAAAGTTTAGCCTATATCCATTCCTTGGAAATCTGCCATCGG 540
Qy 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 541 GATATTAAACCCGAGAACCTCTTTGTTGGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 601 TTTGGAAGTCAAAAGCAGCTGGTCCGAGGAGAACCCAAATGTTTCGTATATCTGTTCTCGG 660
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 661 TACTATAGGGCACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGA 720
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 721 TGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
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QY 147 GluThrValTyrArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIle 166
Db 707 GAGACAGTGTACCGGTGGCCGCCCACTTCACCAAGCCCAAGTTGACCACTCCCTATCCCTC 766
QY 167 TyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGly 186
Db 767 TATGTCAAGGTGTACATGTACCAAGCTCTCCGAGCTTGGCCCTACATCCACTCCAGGGC 826
QY 187 IleCysHisArgAspIleTyrProGlnAsnLeuLeuAspProAspThrAlaValLeu 206
Db 827 GTGTGTACCGCGACATCAAGCCCAAGACCTGCTGGTGAGCCCTGACACTGCTGTCTC 886
QY 207 LysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyr 226
Db 887 AAGCTCTGCGATTTGGCAGTCAAGAGCAGTGGTCCGAGGGGAGGCCCAATGTCTCTAC 946
QY 227 IleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSer 246
Db 947 ATCTGTCTCGCTACTACCGGGCCCAAGCTCATCTTTGGAGCCACTGATTACACTCA 1006
QY 247 SerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIle 266
Db 1007 TCCATCGATTTGGTCAGCTGCTGTGTACTGGCAGAGCTCTCTTGGGCCAGCCATC 1066
QY 267 PheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysValLeuGlyThrPro 286
Db 1067 TTCCTCGGGACAGTGGGTGGACCAAGCTGCTGGAGATCATCAAGGTGCTGGGAACACCA 1126
QY 287 ThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIle 306
Db 1127 ACCGGGAACAAATCCGAGAGATGAACCCCACTACACGAGTTCAAGTTCCTTCAGATT 1186
QY 307 LysAlaHisProTrpThrLysValPheArgProArgThrProGluAlaIleAlaLeu 326
Db 1187 AAAGCTCACCCCTGGACAAAGTGTTCAAATCTCGAAGCGCCGACAGAGCCATCGGCTC 1246
QY 327 CysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAla 346
Db 1247 TGCTCTAGCTGTGGAGTACACCCCACTCTCAAGGCTCTCCCACTTAGAGGCTGTGGC 1306
QY 347 HisSerPheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThr 366
Db 1307 CACAGCTTCTTGATGAACCTGCGATGCTGGGACCCAGCTGCTTACACCCGCCACTT 1366
QY 367 ProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIle 386
Db 1367 CCCCTCTCTCAACTTCAGTGTGGTGAACCTCTCCATCCACCGTCTCTCAACGCCATT 1426
QY 387 LeuIleProProHisAlaArg 393
Db 1427 CTCATCCCTCCTCACTTGAGG 1447

RESULT 9

US-11-266-748A-381459
; Sequence 381459, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266.748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 381459
; LENGTH: 2134
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (49)..(49)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (61)..(61)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73)..(73)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (176)..(255)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1812)..(1878)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2002)..(2002)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2022)..(2022)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2024)..(2024)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2057)..(2057)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2092)..(2092)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-381459

Alignment Scores:

Pred. No.:	1.02e-169	Length:	2134
Score:	1609.00	Matches:	312
Percent Similarity:	86.8%	Conservative:	24
Best Local Similarity:	80.6%	Mismatches:	37
Query Match:	77.3%	Indels:	14
DB:	8	Gaps:	3

US-10-733-816-2 (1-394) x US-11-266-748A-381459 (1-2134)

QY 8 GlyGlyGlyMetSerGlyArgProArgThr---ThrSerPheAlaGluSerCysLysPro 26
|||||
|||||

DB: 8 4 Gaps: 4

US-10-733-816-2 (1-394) x US-11-266-748A-28735 (1-2154)

Qy 5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
 107 CCTTCGGGAGCGCGCCCTCGGGGCTCGGGCAGCGCGAGCTAGCTGTTCGGAG--- 163

Qy 24 CysLysPro-----ValGlnGln 29

Db 164 -----CCCGCGCGGAGCGGAGGCGGGCGGGCCCGGAGGCTCGGCC 217

Qy 30 ProSerAlaPheGlySerMetLys----- 37

Db 218 CCAGGCGGACCGCGCGGAAAGGCATCTGTCTGGGGCCATGGGTGGGGCGTTCGGGGCC 277

Qy 37 ----- 37

Db 278 TCAGCTCCGGGGTGGACCCGCGCGCAGCGGCGGAGGAGCGGAGGCGCGCGCGCA 337

Qy 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49

Db 338 GGCACCTAGCTTCCCGCGCGCGGGGTGAAGCTGGCGGTGACAGCGGAGGTTGACACCA 397

Qy 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGlnValSerTyrThrAspThr 69

Db 398 GTCGTAGCCACTTAGGCCAAGCGCCAGAGCGCTCCCAAGAGTGGCTTACACGACATC 457

Qy 70 LysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuLysCysAspSerGly 89

Db 458 AAAGTGATTGGCAATGGCTCATTTGGGGTGGTGTACAGGCGCTGCGAGAGCAGG 517

Qy 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109

Db 518 GAACCTAGTCCCATCAAGAGGTTCTCCAGGACAGAGGTTCAAGAACCGAGAGCTGAG 577

Qy 110 IleMetArgLysLeuAspHisCysAenIleValArgLeuArgTyrPhePheTyrSerSer 129

Db 578 ATCATGCTGAAGCTGACCACTGCAATATTGTGAGGCTGAGATATCTTTTCTACTCCAGT 637

Qy 130 GlyGluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrVal 149

Db 638 GCGGAGAAGAAACACAGAGCTTTACCTAAATCTGGTGTGAATATGTGCCCGAGACAGTG 697

Qy 150 TyrArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169

Db 698 TACGGGTGGCCCGCCACCTTACCAGGCGCAAGTGTACCATCCCTATCTCTATGTCAAG 757

Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyLeCysHis 189

Db 758 GTGTACATGTATACAGCTTTCGCGAGCTTGGCTATACATCCATCCCGGCGGTGTCTAC 817

Qy 190 ArgAspIleLysProGlnAenLeuLeuAspProAspThrAlaValLeuLysLeuCys 209

Db 818 CCGGACATCAAGCCCGCAGAACCTGTGTGGTGGGACCTGTGACCTGTCTCAAGCTCTGC 877

Qy 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAenValSerTyrIleCysSer 229

Db 878 GATTTTGGCAGTGCAAAGCAGTTGGTCCGAGGGAGCCCAATGTCTCTACATCTGTCT 937

Qy 230 ArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAsp 249

Db 938 CGCTACTACCGGCGCCAGAGCTCATCTTTGGAGCCACTGATTACACCTCATCCATCAT 997

Qy 250 ValTyrSerAlaGlyCysValLeuAlaGluLeuLeuLeuLeuGlyGlnProIlePheProGly 269

Db 998 GTTTTGGTCACTGGCTGTGTACTGGCAGAGCTCTCTTGGGCGAGCCCATCTTCCCTGG 1057

Qy 270 AspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGlu 289

Db 1058 GACAGTGGGTGGACAGCTGGTGGAGATCATCAAGGTGCTGGGAACACCAACCCGGGAA 1117

Qy 290 GlnIleArgGluMetAenProAenTyrThrGluPheLysPheProGlnIleLysAlaHis 309

Db 1118 CAAATCCGAGATGAACCCCACTACACGGAGTTCAAGTTCCCTCAGATTAAAGCTCAC 1177

Qy 310 ProTyrThrLysValPheArgProArgThrProGluAlaIleAlaLeuLysSerArg 329

Db 1178 CCTGAGCAAAAGGTGTCAATCTCGAACCGCGCAGAGGCATCGCGCTCTGTCTTAGC 1237

Qy 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349

Db 1238 CTGCTGGAGTACACCCCATCTCAAGGCTCTCCCACTAGAGGCTGTGCGCACAGCTTC 1297

Qy 350 PheAspGluLeuArgAspProAenValLysHisProAenGlyArgAspThrProAlaLeu 369

Db 1298 TTTGATGAACCTCGATGTCTGGGAACCCAGCTGCTTAACAACCCGCCCATCTCCCTCTC 1357

Qy 370 PheAenPheThrThrGlnGluLeuSerSerAenProProLeuAlaThrIleLeuIlePro 389

Db 1358 TTCACCTTCAGTGTGGTGAACCTCTCCATCCACACGCTCTCTCAACGCCATCTCATCCCT 1417

Qy 390 ProHisAlaArg 393

Db 1418 CCTCACTTGAGG 1429

RESULT 12

US-10-553-520-84

; Sequence 84, Application US/10553520

; Publication No. US2006018885A1

; GENERAL INFORMATION:

; APPLICANT: Bodian, Dale

; APPLICANT: Daouti, Sherif

; APPLICANT: Kumar, Chandrika

; APPLICANT: Lataario, Brian

; APPLICANT: Quintavalla, Joseph

; TITLE OF INVENTION: High throughput functional genomic

; TITLE OF INVENTION: screening methods for osteoarthritis

; FILE REFERENCE: 4-33178

; CURRENT APPLICATION NUMBER: US/10/553,520

; CURRENT FILING DATE: 2005-10-14

; PRIOR APPLICATION NUMBER: 60/463,933

; PRIOR FILING DATE: 2003-04-18

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 84

; LENGTH: 2169

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-553-520-84

Alignment Scores:

Pred. No.: 1,05e-169 Length: 2169

Score: 1609.00 Matches: 319

Percent Similarity: 77.3% Conservative: 24

Best Local Similarity: 71.8% Mismatches: 43

Query Match: 77.3% Indels: 58

DB: 6 Gaps: 4

US-10-733-816-2 (1-394) x US-10-553-520-84 (1-2169)

Qy 5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23

Db 130 CCTTCGGGAGCGCGCCCTCGGGGCTCGGGGCGCGGAGCTAGCTGTTCGGAG--- 186

Qy 24 CysLysPro-----ValGlnGln 29

Db 187 -----CCCGCGGCGGAGCGGAGGCGCGCGCGCGCGCGGCTCGGCTCCGGC 240

Qy 30 ProSerAlaPheGlySerMetLys----- 37

Db 241 CCAGGCGGACCGCGCGGCGGAAAGGCATCTGTGGGGCCATGTGGTGGGGCGTTCGGGGCC 300

Qy 37 ----- 37

Db 301 TCAGCTCCGGGGTGGACCCCGCGCGCAGCGCGGAGGAGCGAGGCGCGCGCGCA 360

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QY 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 361 GGCACCTAGCTCCCGCGCGCGGCGTGAAGCTGGCGTACAGCGGGAAGGTGACACA 420
QY 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThr 69
Db 421 GTCGTAGCCACTTAGGCCAAGGCCAGCGCTCCCAAGAGTGGCTTACACGGACATC 480
QY 70 LysValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGly 89
Db 481 AAGTGTATGGCAATGGCTCATTTGGGTCGTGTACCGACCGCTGGCAGAGACCGAG 540
QY 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109
Db 541 GAATAGTCCCACTCAAGAGGTTCTCCAGGACAAGAGGTTCAAGAACCGAGAGCTGCAG 600
QY 110 IleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSer 129
Db 601 ATCATGGTAAAGCTGGACCACTGCATATTTGTGAGGCTGAGATACATTTTCTACTCCAGT 660
QY 130 GlyGluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149
Db 661 GCGGAGAAGAAGACGAGCTTTACCTAAATCTGGTGTGAATATGTGCCCGAGACAGTG 720
QY 150 TyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
Db 721 TACCGGGTGGCCGCCCACTTCACCAAGGCCAAGTTGACCATCCCTATCTCTATGTCAAG 780
QY 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189
Db 781 GTGTACATGTACAGCTCTTCCGAGCTTGGCCGTACATCCACTCCAGGGCGTGTCTAC 840
QY 190 ArgAspLysLysProGlnAsnLeuLeuLeuAspProAspThrAlaValLeuLysLeuCys 209
Db 841 CGCGACATCAAGCCCAAGACCTGTGTGGAGCCCTGACACTGTGTCTCAAGCTCTGC 900
QY 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer 229
Db 901 GATTTTGGCAGTCAAGACAGTGTGTCCGAGGGGAGGCCCAATGTCTCTCATCTGTCTCT 960
QY 230 ArgTyrTyrArgAlaProGluLeuIlePheGlyValaThrAspTyrThrSerSerIleAsp 249
Db 961 CGCTACTACCGGGCCCGCAGAGCTCATCTTTGGAGCCACTGATTACACTCATCATCAT 1020
QY 250 ValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGly 269
Db 1021 GTTTGGTCACTGGCTGTGTACTGGCAGAGCTCTCTTGGGCCAGCCCATCTTCCCTGGG 1080
QY 270 AspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGlu 289
Db 1081 GACAGTGGGTGGACCAAGCTGGTGGAGATCATCAAGGTGTGGAAACCAACCCCGGAA 1140
QY 290 GlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHis 309
Db 1141 CAAATCCGAGAGATGAACCCCACTACACGAGTTCAAGTTCCCTCAGATTAAGCTCAC 1200
QY 310 ProTrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArg 329
Db 1201 CCCTGGACAAAGGTGTTCAAACTCTCGAAGCCGCGCAGAGCCATCGCGCTCTGTCTTAGC 1260
QY 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
Db 1261 CTGCTGAGTACACCCCATCTCAAGGCTCTCCCACTAGAGGCTGTGGCAGAGCTTC 1320
QY 350 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu 369
Db 1321 TTTGATGAATGTGATGTCTGGGAACCCAGCTGGCTTAACAACCCGCTCTCCCTCTC 1380
QY 370 PheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIlePro 389
Db 1381 TTCAACTTCAGTGTGGTGAACCTCTCCATCCAAACCGTCTCTCAACGCGCATCTCATCCCT 1440
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QY 390 ProHisAlaArg 393
Db 1441 CTTCACTTGAGG 1452

RESULT 13
US-11-266-748A-56261
; Sequence 56261, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 56261
; LENGTH: 2200
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-56261

Alignment Scores:
Pred. No.: 1,07e-169 Length: 2200
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 24
Best Local Similarity: 71.8% Mismatches: 43
Query Match: 77.3% Indels: 58
DB: 8 Gaps: 4

US-10-733-816-2 (1-394) x US-11-266-748A-56261 (1-2200)

QY 5 ProMetGluGlyGly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
Db 135 CCTTCGGAGAGCGGCCCTCGGGGCTCGGGCAGCGCGAGCTAGCTCGTTTCGGGAG--- 191
QY 24 CysLysPro-----ValGlnGln 29
Db 192 -----CCCGCGCGGAGCGGAGGCGGCGGCGGCGGCGGCTCGGCTCCGGC 245
QY 30 ProSerAlaPheGlySerMetLys----- 37
Db 246 CCAGCGGCGCAGCGCGCGGAAAGCATCTGTCCGGGCCATGTGGTGGGCGCTCGGGGCC 305
QY 37 ----- 37
Db 306 TCGAGCTCCGGGGGTGGACCCCGCGCAGCGGAGGAGGAGCGGAGCGGCGGCGGCGCA 365
QY 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 366 GGCACCTAGCTTCCCGCGCGCGGGGTGAAGCTGGCGCTGACAGCGGGAAGGTGACACA 425
QY 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThr 69
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Db 426 GTCTAGCACTCTAGGCCAAGGCCAGAGCGCTCCCAAGAGTGCGTTACAGGCATC 485
Qy 70 LysValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGly 89
Db 486 AAGTGTATTGGCAATGGCTCATTTGGGCTCGTGTACAGGCACGGCTGGCAGACCCAGG 545
Qy 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAenArgGluLeuGln 109
Db 546 GAACATAGTCCCAATCAAGAGGTTCTCCAGACAAGAGGTTCAAGAACCCGAGAGCTCAG 605
Qy 110 IleMetArgLysLeuAspHisCysAenIleValArgLeuArgTyrPhePheTyrSerSer 129
Db 606 ATCATGCGTAAGCTGGACCACTGCAATATTGTGAGGCTGAGATACCTTTTCTACTCCAGT 665
Qy 130 GlyGluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrVal 149
Db 666 GCGCAGAAGAAGACGAGCTTTACCTAAATCTGTGTGCTGGAATATGTGCCGAGACAGTG 725
Qy 150 TyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
Db 726 TACCGGGTGGCCCGCCACTTCCCAAGGCCAAGTTGACCATCCTATCTCTATGTCAAG 785
Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189
Db 786 GTGTACATGTACCAGCTCTTCCGAGCTTGGCCCTACATCCACTCCAGGGCGGTGTCTAC 845
Qy 190 ArgAspLysProGlnAenLeuLeuLeuAspProAspThrAlaValLeuLysLeuCys 209
Db 846 CGCGACATCAAGCCCCAGAACCTGTGTGGAGCCCTGACACTGTGTCTCTCAAGCTCTGC 905
Qy 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAenValSerTyrIleCysSer 229
Db 906 GATTTTGGCAGTGCACAGCAGTGTGGTCCGAGGGAGGCCAATGTCTCTACATCTGTCT 965
Qy 230 ArgTyrTyrArgAlaProGluLeuIlePheGlyValAlaThrAspTyrThrSerSerIleAsp 249
Db 966 CGCTACTACCGGGCCCCAGAGCTCACTTTGGAGCCACTGATTACACTCATCATCATCAT 1025
Qy 250 ValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGly 269
Db 1026 GTTTGGTCACTGGCTGTGTACTGGCAGAGCTCTCTTTGGCCAGCCCATCTTCCCTGGG 1085
Qy 270 AspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGlu 289
Db 1086 GACAGTGGGTGGACCACTGCTGGAGATCATCAAGGTGTGGGAACACCAACCCGGGAA 1145
Qy 290 GlnIleArgGluMetAenProAenTyrThrGluPheLysPheProGlnIleLysAlaHis 309
Db 1146 CAATCCGAGAGATGAACCCCACTACAGGAGTTCAAGTTCCCTCGATTAAGCTCTAC 1205
Qy 310 ProTrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArg 329
Db 1206 CCCTGGACAAAGTGTTCAAATCTCGAACCGCCGAGAGCCATCGGCTCTGCTTAGC 1265
Qy 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
Db 1266 CTGCTGGAGTACACCCCATCTCAAGGCTCTCCCCACTAGAGGCTGTGGCCACAGCTTC 1325
Qy 350 PheAspGluLeuArgAspProAenValLysHisProAenGlyArgAspThrProAlaLeu 369
Db 1326 TTTGATGAATCGGATGCTGGGAACCCAGCTGCTTAACACCGCCCACTTCCCCCTCTC 1385
Qy 370 PheAenPheThrThrGlnGluLeuSerSerAenProProLeuAlaThrIleLeuPro 389
Db 1386 TTCAACTTCACTGCTGGTGAATCTTCCATCCAACCGTCTCTCAACGCCATCTCATCCCT 1445
Qy 390 ProHisAlaArg 393
Db 1446 CCTCACTTGAGG 1457

RESULT 14

US-10-795-135-4

; Sequence, 4, Application US/10795135

; Publication No. US20060099599A1
; GENERAL INFORMATION:
; APPLICANT: HEBERLEIN, ULRIKE
; APPLICANT: WOLFE, FRED
; TITLE OF INVENTION: THE ROLE OF GLYCOGEN SYNTHASE KINASE-3 AND TETRASPANINS IN
; TITLE OF INVENTION: ETHANOL-INDUCED BEHAVIORS
; FILE REFERENCE: 316T-002010US
; CURRENT APPLICATION NUMBER: US/10/795,135
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US60/452,486
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: Drosophila sp.
US-10-795-135-4

Alignment Scores: 7.43e-168 Length: 1545
Pred. No.: 1590.50 Matches: 305
Score: 88.0% Conservative: 32
Percent Similarity: 79.6% Mismatches: 41
Best Local Similarity: 76.4% Indels: 5
Query Match: 6 Gaps: 4
DB:

US-10-733-816-2 (1-394) x US-10-795-135-4 (1-1545)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
Db 1 ATGAGCGGTGCTCCAGAACTTCTCTCTCCGCGAGGGCAACAAA-----CAGTCGCCG 54
Qy 31 Ser---AlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThr 49
Db 55 AGTTTGGTGTGGCGCGCTCAAAACATGC--AGTCGCATGGTCTTAAATCACAACA 111
Qy 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThr 69
Db 112 GTTGTGTCAACACCCGCCAAGGCACCGATCGCGTACAGAGGTCTCTATACAGACACA 171
Qy 70 LysValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGly 89
Db 172 AAGTCTATCGGCATCGCAGCTTCGGCGTGTTCAGGCAAGCTCTCGGATACCCGC 231
Qy 90 GluLeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAenArgGluLeuGln 109
Db 232 GAACCTGGTCATCAAAAAGTTTACAGACAGACGATTTAAGATCGGAAATTCGAA 291
Qy 110 IleMetArgLysLeuAspHisCysAenIleValArgLeuArgTyrPhePheTyrSerSer 129
Db 292 ATAATCGCAAAATGGAGCATTTGTAATATTGTGAAGCTTTGTACTTTTCTATTTCAGT 351
Qy 130 GlyGluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrVal 149
Db 352 GGTGAAGACGATGATGAAGTATTTTGAATTTTGTCTCGAATATATACAGAAACCGTA 411
Qy 150 TyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
Db 412 TACAAAGTGGCTGCCAATATGCAAAACCAACCAACGATCAACATCACTTATTTCGG 471
Qy 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189
Db 472 CTCTACATGTATCAACTGTTTCAGAGTTTGGCCCTACATCCACTCGCTGGGCAATTTGCCAT 531
Qy 190 ArgAspLysProGlnAenLeuLeuLeuAspProAspThrAlaValLeuLysLeuCys 209
Db 532 CGTGATATCAAGCCGAGATCTTCTGCTGATCCGAGACCGCTGTGCTGAAGCTCTGT 591
Qy 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAenValSerTyrIleCysSer 229
Db 592 GACTTTGGACAGCCCAACAGCTGTGTCAGCGGCGAGCCGAAATGTATCTATATCTGCTCC 651

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 00:35:50 ; Search time 5832 Seconds
(without alignments)
6480.268 Million cell updates/sec

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Perfect score: 2081
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pcpt -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
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2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
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2	2024	97.3	AR270851 Sequence
3	2024	97.3	AX777402 Sequence

4	2024	97.3	1389	5	HUMGLSYKIN	L33801 Human prote
5	2015	96.8	1525	6	RNTAU	AF156099 Mus muscu
6	2015	96.8	1535	6	ARF156099	AR059074 Sequence
7	2015	96.8	1972	2	AR059074	AR097211 Sequence
8	2015	96.8	1972	2	AR097211	BD181611 Method of
9	2015	96.8	1972	2	BD181611	E08007 DNA encodin
10	2015	96.8	1972	2	E08007	BC006936 Mus muscu
11	2015	96.8	2841	6	BC006936	AB066114 Mus muscu
12	2015	96.8	8304	6	AB066114	AX821914 Sequence
13	2013	96.7	1231	2	AX821914	AX701656 Sequence
14	2013	96.7	1263	2	AX701656	CF536510 Homo sapi
15	2013	96.7	1263	5	CF536510	AX701653 Sequence
16	2013	96.7	1389	2	AX701653	BC006936 Mus muscu
17	2013	96.7	1503	6	BC006936	BC012760 Homo sapi
18	2013	96.7	1815	2	BC012760	X53428 Rat mRNA fo
19	2013	96.7	2374	5	BC012760	AY32021 Spermophi
20	2012	96.7	1474	6	RNGSK3B	AR059073 Sequence
21	2010	96.6	2088	2	AR059073	AR097210 Sequence
22	2010	96.6	2088	2	AR097210	E08052 cDNA encodi
23	2010	96.6	2088	2	E08052	AY32021 Spermophi
24	2008	96.5	1437	6	AY32021	AY335634 Synthetic
25	1996.5	95.9	1302	8	AY335634	CQ986514 Sequence
26	1996.5	95.9	1639	2	CQ986514	CQ981289 Sequence
27	1996.5	95.9	1639	2	CQ981289	CS160757 Sequence
28	1996.5	95.9	1639	2	CS160757	BC000251 Homo sapi
29	1996.5	95.9	1639	5	BC000251	AB032265 Danio rer
30	1959	94.1	2321	11	AB032265	LJ223502 Danio rer
31	1959	94.1	2624	11	AB032265	L38492 Xenopus lae
32	1931	92.8	4394	11	XELGSK	BC108581 Xenopus l
33	1931	92.8	2090	11	BC108581	U31862 Xenopus lae
34	1923	92.4	1263	11	XLU31862	AJ223501 Danio rer
35	1704.5	81.9	2983	11	DAR223501	BC056332 Danio rer
36	1704.5	81.9	3040	11	BC056332	BC065952 Danio rer
37	1704.5	81.9	3100	11	BC065952	AB032264 Danio rer
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40	1666.5	80.1	2708	13	AB031544	AB211133 Clona int
41	1666.5	80.1	2726	13	AB211133	CQ719548 Sequence
42	1663	79.9	1027	2	CQ719548	DD210782 KINASES A
43	1634.5	78.5	1698	2	DD210782	AY624076 Lytechinu
44	1632	78.4	1245	13	AY624076	AJ222641 Paracentr
45	1614	77.6	6129	13	PLAJ641	

ALIGNMENTS

RESULT 1	AR262205	AR262205	Sequence 3 from patent US 6323029.	1389 bp	DNA	linear	PAT 29-JAN-2003
LOCUS	AR262205	Sequence 3 from patent US 6323029.					
DEFINITION	AR262205	Sequence 3 from patent US 6323029.					
ACCESSION	AR262205	Sequence 3 from patent US 6323029.					
VERSION	AR262205.1	GI:28073593					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1389)						
AUTHORS	Butler, M.M., McKay, R., Monia, B.P. and Wyatt, J.						
TITLE	Antisense modulation of glycogen synthase kinase 3 beta expression						
JOURNAL	Patent: US 6323029-A 3 27-NOV-2001.						
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source	1..1389						
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Alignment Scores:							
Pred. No.:	1.51e-184	Length:	1389				
Score:	2024.00	Matches:	384				
Percent Similarity:	100.0%	Conservative:	0				
Best Local Similarity:	100.0%	Mismatches:	0				
Query Match:	97.3%	Indels:	0				

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Db 40 ATGTCAGGCGCGCCAGAACCACTCTTTGGGAGAGCTGCAAGCGGTGCAGCAGCCT 99
Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAGTTAGCAGACACAAGACGCGCAGAGGTGACACAGTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTGGCGAGGTGCAGACAGGCCCAAGAGTTCAGCTATACAGACATAAA 219
Qy 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTCCAGGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAenArgGluLeuGlnIle 110
Db 280 CTGGTCGCCATCAAGAAGATTATGCAGACAAAGATTAAAGAAATCGAGAGCTCCAGATC 339
Qy 111 MetArgLysLeuAspHisCysAenIleValArgLeuArgTyrPhePheTyrSerSerGly 130
Db 340 ATGAGAAAGCTAGATCATCTGTAACATAGTCCGATTGGTTATTTCTTCTACTCCAGTGGT 399
Qy 131 GluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAAACAGTATAC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
Db 460 AGAGTTGCCAGACACTATAGTCAGGCCAAACAGACGCTCCCTGTGATTATGTCAAGTTG 519
Qy 171 TyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
Db 520 TATATGATCAGCTGTTCGGAAGTTTAGCTTATATCATCTTCTTTGGAAATCTGCCATCGG 579
Qy 191 AspIleLysProGlnAenLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210
Db 580 GATATTAAACCGCAGAACCTCTTTGTGATCCTGTACTGCTGTATTAAAACTCTGTGAC 639
Qy 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAenValSerTyrIleCysSerArg 230
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Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyValaThrAspTyrThrSerSerIleAspVal 250
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Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
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Qy 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
Db 940 TGGACTAAGGCTCTTCCGACCCCGAACTCCACGGAGGCAATTGCACTGTGTAGCCGCTG 999
Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
Db 1000 CTGGAGTATACACCAACTGCCCGACTAACCACTAGCAAGCTGTGTGACATTCATTTTTT 1059
Qy 351 AspGluLeuArgAspProAenValLysHisProAenGlyArgAspThrProAlaLeuPhe 370
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Db 1120 AACTTCACCACTCAAGAACTGTCAAGTAATCCACCTCTGGCTACCATCTTATTCTCTCT 1179
Qy 391 HisAlaArgIle 394
Db 1180 CATGCTCGGATT 1191
RESULT 2
LOCUS AR270851 1389 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1414 from patent US 6500938.
ACCESSION AR270851
VERSION AR270851.1 GI:29702085
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1389)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1414 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
WOX;
FEATURES
source 1. .1389
/organism="unknown"
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Alignment Scores: 1.51e-184 Length: 1389
Pred. No.: 2024.00 Matches: 384
Score: 2024.00 Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 97.3% Gaps: 0
DB: 2
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Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTGGCGAGGTGCAGACAGGCCCAAGAGTTCAGCTATACAGACATAAA 219
Qy 71 ValIleGlyAenGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
Db 220 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCAACTTTGTGATTCCAGGAA 279
Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAenArgGluLeuGlnIle 110
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Qy 131 GluLysLysAspGluValTyrLeuAenLeuValLeuAspTyrValProGluThrValTyr 150
Db 400 GAGAGAAAGATGAGGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAAACAGTATAC 459
Qy 151 ArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
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Db 520 TATATGTATCAGCTGTTCGGAAGTTTAGCCCTATATCATTCCTTTGGAAATCGCCATCGG 579
Qy 191 AspIleIysProGlnAsnLeuLeuAspProAspThrAlaValLeuIysLeuCysAsp 210
Db 580 GATATTAAACCGCAGAACCTCTTGTGGATCCTGTACTGCTGTATTAATAAATCTGTGAC 639
Qy 211 PheGlySerAlaIysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
Db 640 TTGTGAAGTCCAAAGCAGCTGTTCGAGGAGAACCCCAATGTTTCGTATATCTGTCTCG 699
Qy 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
Db 700 TACTATAGGCGCACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGATGTA 759
Qy 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
Db 760 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTACTAGGACCAACCAATATTATTCAGGGGAT 819
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Qy 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
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Db 1060 GATGAATTCAGGGACCCAAATGTCAAAATCCAAATCCAAATGGGGAGACACACCTGCACCTTC 1119
Qy 371 AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIleProPro 390
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LOCUS AX777402 1389 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 256 from Patent WO03040301.
ACCESSION AX777402
VERSION AX777402.1 GI:32694471
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Deak, P., Frensz, L., Glover, D. and Midgley, C.
TITLE Cell cycle progression proteins
JOURNAL Patent: WO 03040301-A 256 15-MAY-2003;
Cyclacel Limited (GB)
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Alignment Scores:

Pred. No.: 1-51e-184 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 2 Gaps: 0

US-10-733-816-2 (1-394) x AX777402 (1-1389)

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Qy 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
Db 100 TCAGCTTTTGGCAGCATGAAGATTAGCAGACAGACGCGCAGCAAGGTGACACAGTG 159
Qy 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
Db 160 GTGGCAACTCTCTGGCAGGCTCCAGACAGGCCCAAGAGCTCAGCTATACAGACACTAAA 219
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Db      1000  CTGGAGTATACACCAACTGCCGACTAAACACCACTGGAAGCTGTGCACATTCATTTTTT 1059
Qy      351  AspGluLeuArgAspProAlaValHisProAsnGlyArgAspThrProAlaLeuPhe 370
Db      1060  GATGAATTACGGGACCCAAATGTCAAACATCCAAATCGGGGAGACACACCTGCACCTTC 1119
Qy      371  AsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
Db      1120  AACTTCACCACTCAAGACTGTCAAGTATATCCACTCTGGCTACCATCCTTATTCCTCT 1179
Qy      391  HisAlaArgIle 394
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RESULT 4
HUMGLSYKIN HUMGLSYKIN 1389 bp mRNA linear PRI 16-MAY-1995
LOCUS      Human protein kinase mRNA, complete cds.
DEFINITION L33801
VERSION     L33801.1 GI:592336
KEYWORDS   glycogen synthase kinase 3; protein kinase.
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 1389)
AUTHORS    Stambolic,V. and Woodgett,J.R.
TITLE      Mitogen inactivation of glycogen synthase kinase-3 beta in intact
            cells via serine 9 phosphorylation
JOURNAL    Biochem. J. 303 (Pt 3), 701-704 (1994)
PUBMED     7980435
COMMENT     Original source text: Homo sapiens (library: lambda ZAP) cDNA to
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            ORIGIN

Alignment Scores:
Pred. No.: 1,51e-184 Length: 1389
Score: 2024.00 Matches: 384
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.3% Indels: 0
DB: 5 Gaps: 0

US-10-733-816-2 (1-394) x HUMGLSYKIN (1-1389)
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Db      40  ATGTGAGGCGCCAGAACACACCTCTCTTTCGGGAGAGCTGCAAGCCGTGAGCAGCCT 99
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Db      100  TCAGCTTTTGGCAGCATGAAGTTAGCAGAGACAAGGACGGCAGCAAGGTGACAACAGTG 159
Qy      51  ValAlaThrProGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLys 70
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Qy      71  ValIleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGlu 90
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Db      400  GAGAGAAAGATGAGGCTCTATCTTAATCTGTGTGCTGACTATGTTCCGGAACAGATATAC 459
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QY 391 HisAlaArgile 394

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RESULT 5

RNTAU 1525 bp mRNA linear ROD 18-APR-2005

LOCUS R. norvegicus mRNA for tau protein kinase I.

DEFINITION X73653.1 S63460

ACCESSION X73653.1 GI:402651

VERSION

KEYWORDS tau protein kinase.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 1525)

AUTHORS Ishiguro, K., Shiratsuchi, A., Sato, S., Omori, A., Arioka, M., Kobayashi, S., Uchida, T. and Imahori, K.

TITLE Glycogen synthase kinase 3 beta is identical to tau protein kinase I generating several epitopes of paired helical filaments

JOURNAL FEBS Lett. 325 (3), 167-172 (1993)

PUBMED 7686508

REFERENCE 2 (bases 1 to 1525)

AUTHORS Kobayashi, S., Ishiguro, K., Omori, A., Takamatsu, M., Arioka, M., Imahori, K. and Uchida, T.

TITLE A cdc2-related kinase PSSALRE/cdk5 is homologous with the 30 kDa subunit of tau protein kinase II, a proline-directed protein kinase associated with microtubule

JOURNAL FEBS Lett. 335 (2), 171-175 (1993)

PUBMED 8253190

REFERENCE 3 (bases 1 to 1525)

AUTHORS Uchida, T.

TITLE Direct Submission

JOURNAL Submitted (17-AUG-1993) T. Uchida, Mitsubishi Kasei, Institute of Life Sciences, 11 Minamiooya Machida-shi, Tokyo 194, JAPAN

COMMENT On May 10, 2005 this sequence version replaced gi:393351.

FEATURES

source 1..1525

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CDS

Alignment Scores:

Pred. No.: 1,25e-183 Length: 1525

Score: 2015.00 Matches: 386

Percent Similarity: 98.0% Conservative: 0

Best Local Similarity: 98.0% Mismatches: 2

Query Match: 96.8% Indels: 6

DB: Gaps: 1

US-10-733-816-2 (1-394) -x RNTAU (1-1525)

QY 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20

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QY 21 AlaGluSerCysLysProValGlnGlnProSerAlaPheGlySerMetLysValSerArg 40

Db 170 GCGGAGAGCTGCAAGCCAGTGCAGAGCCTTCAGCTTTTGGTAGCATGAAGTTAGCAG 229

QY 41 AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60

Db 230 GATAAAGATGGCAGCAAGGTAAACACAGTGTGTGCAACTCTCGACAGGGTCTCTGACAG 289

QY 61 ProGlnGluValSerTyrThrAspThrLysValLleGlyAsnGlySerPheGlyValVal 80

Db 290 CCACAGAAAGTCAAGTACAGACACTAAAGTCATTGGAAANTGGTCAATTTGGTGGTA 349

QY 81 TyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaLleLysLysValLeuGlnAsp 100

Db 350 TATCAAGCCAACTTTGTGACTCAGGAGAACTGTGTGCCCATCAAGAAAGTTCTTCAGGAC 409

QY 101 LysArgPheLysAsnArgGluLeuGlnLleMetArgLysLeuAspHisCysAsnLleVal 120

Db 410 AAGCGATTAAAGAACCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTC 469

QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140

Db 470 CGATTGCGGTATTCTTCTACTCGAGTGGCAGAGAAAGATGAGGTCTACCTTAACCTG 529

QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLys 160

Db 530 GTGCTGGACTATGTTCCGGAACAGTGTACAGAGTCCAGACACTATAGTCGAGCCAAG 589

QY 161 GlnThrLeuProValLleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180

Db 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTATACCAAGCTGTTTCAAGAGTCTAGCC 649

QY 181 TyrIleHisSerPheGlyLleCysHisArgAspLysProGlnAsnLeuLeuAsp 200

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Db 710 CCTGATACAGCTGTATTAAACTCTCGGACTTTGGAGTGCNAAGCAGCTGGTCCGAGGA 769

QY 221 GluProAsnValSerTyrLleCysSerArgTyrTyrArgAlaProGluLeuLlePheGly 240

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Db 830 GCCACCGATTACACGCTTAGTAGTAGTATGCTGTGCAGGCTGTGTGTGGTGAATG 889

QY 261 LeuLeuGlyGlnProLlePheProGlyAspSerGlyValAspGlnLeuValGluLleIle 280

Db 890 TTGCTAGGACAACCAATATTTCTCGGACAGTGTGTGGATCAGTTGTGGAAATATA 949

QY 281 LysValLeuGlyThrProThrArgGluGlnLleArgGluMetAsnProAsnTyrThrGlu 300

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QY 301 PheLysPheProGlnLleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320

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QY 361 ProAenGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn 380
Db 1190 CCAATGGGGAGACACACTGCGCTCTCAACTTTACCACTCAAGACTGTCAAGTAAC 1249
QY 381 ProProLeuAlaThrLeuLeuLeuProProHisAlaArgile 394
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RESULT 6
AF156099 1535 bp mRNA linear ROD 24-FEB-2000
LOCUS Mus musculus glycogen synthase kinase 3 beta mRNA, complete cds.
DEFINITION AF156099
ACCESSION AF156099
VERSION AF156099.2 GI:7025914
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1535)
Salameh,W.A., Guo,T.B., Chan,K.C. and Mitchell,A.P.
Testicular expression and hormonal control of glycogen synthase
kinase 3, a homologue of yeast Rim1
Unpublished
REFERENCE 2 (bases 1 to 1535)
Salameh,W.A., Guo,T.B., Chan,K.C. and Mitchell,A.P.
Direct Submission
AUTHORS Submitted (02-JUN-1999) Division of Endocrinology, Department of
Medicine, Harbor-UCLA Medical Center, 1000 West Carson Street,
Torrance, CA 90502, USA
REFERENCE 3 (bases 1 to 1535)
Salameh,W.A., Guo,T.B., Chan,K.C. and Mitchell,A.P.
Direct Submission
AUTHORS Submitted (24-FEB-2000) Division of Endocrinology, Department of
Medicine, Harbor-UCLA Medical Center, 1000 West Carson Street,
Torrance, CA 90502, USA
REMARK Sequence update by submitter
COMMENT On Feb 24, 2000 this sequence version replaced gi:5070699.
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SVYRAPLELFGATDVTSSIDVMSAGCVLAELLGQPIRPDGSVQDLVBEIIKVLGTP
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ORIGIN
Alignment Scores:
Pred. No.: 1,26e-183 Length: 1535
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: Gaps: 1

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US-10-733-816-2 (1-394) x AF156099 (1-1535)
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QY 21 AlaGluSerCysIysProValGlnProSerAlaPheGlySerMetIysValSerArg 40
Db 197 GCGAGAGCTGCAAGCCAGTCAGCAGCCTTTCAGCTTTTGTAGCATGAAGATTAGCAGA 256
QY 41 AspLysAspGlySerLysValThrThrValAlaLaThrProGlyGlnGlyProAspArg 60
Db 257 GATAAGATGGCAGCAAGGTAAACCACAGTAGTGGCAACTCTTGGCCAGGCTCTGACAGG 316
QY 61 ProGlnGluValSerTyrThrAspThrLysValLleGlyAsnGlySerPheGlyValVal 80
Db 317 CCACAGGAAGTCAGTTTATACAGACACGAAGTGATTTGGAATGGATCATTTGGTGTGGTA 376
QY 81 TyrGlnAlaIysLeuCysAspSerGlyGluLeuValAlaLleIysLysValLeuGlnAsp 100
Db 377 TATCAAGCCAAACTTTGTGATTCTGGAGAACTGGTTGCCATCAAGAAAGTTCTACAGGAC 436
QY 101 LysArgPheLysAsnArgGluLeuGlnLleMetArgLysLeuAspHisCysAsnLleVal 120
Db 437 AAGCGATTTAAGAACCGAGAGCTCCAGATCATGAGAAAGCTAGACCACCTGTAAACATAGTC 496
QY 121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
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QY 141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160
Db 557 GTGCTGGACTATGTTCCGGAGACAGTGTACAGAGTCGCCAGACACTATATAGTCGAGGCAAG 616
QY 161 GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
Db 617 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTATCATCAGCTGTTCAAGAGTCTAGCC 676
QY 181 TyrIleHisSerPheGlyLysCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
Db 677 TATATCCATTCCTTTGGAAATCTGCCATCGAGACATTTAAACCCAGAACCTCTTTGTTGGAT 736
QY 201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
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QY 221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuLlePheGly 240
Db 797 GAGCCCAATGTTTCATATATCTGTTCTCGTACTACAGGGCCACACAGATTGATCTTTTGA 856
QY 241 AlaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu 260
Db 857 GCCACTGATTTACACGTCACAGTATAGATGTATGCTCTGCAGGCTGTGTGTTGGCTGAATTG 916
QY 261 LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluLle 280
Db 917 TTGCTTAGGACAACAATATTTCTGGGACAGTGGTGGATCAGTTGGTGGAAATAATA 976
QY 281 LysValLeuGlyThrProThrArgGluGlnLleArgGluMetAsnProAsnTyrThrGlu 300
Db 977 AAGTCTCTAGGAACACCAACAGGGAGCAAAATTAGAGAAATGAACCAAAATTATACAGAA 1036
QY 301 PheLysPheProGlnLleLysAlaHisProTyrThrLysValPheArgProAsnThrPro 320
Db 1037 TTCAAAATTCCTCAAAATCAAGGCACATCTCTGGACAAAGGTCTTTCGGGCCCAACTCCA 1096
QY 321 ProGluAlaLleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr 340
Db 1097 CCAGAGGCAATTGCATCTGTGACCCCTGTCTGTGAGGTACACACTACCGCCCGGCTAACA 1156
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Db      1217 CCAATGGGGGAGACACACCTGCACCTCTTCAACTTTTACCACCTCAAGAACTGTCAAGTAA 1276
Qy      381 ProProLeuAlaThrIleLeuIleProProHisAlaArgile 394
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RESULT 7
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LOCUS      AR059074 1972 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5837853.
ACCESSION AR059074
VERSION    AR059074.1 GI:5984651
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1972)
AUTHORS    Takashima,A., Hoshino,T., Imahori,K., Saito,K.-i., Shiratsuchi,A.
TITLE      Preventive or therapeutic agents for alzheimers disease a screening
            method of alzheimers disease and tau-protein kinase I originated
            from human being
JOURNAL    Patent: US 5837853-A 2 17-NOV-1998;
FEATURES   Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      1.75e-183 Length:      1972
Score:          2015.00 Matches:      386
Percent Similarity: 98.0% Conservatives: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match:      96.8% Indels:      6
DB:              2 Gaps:      1

US-10-733-816-2 (1-394) x AR059074 (1-1972)

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Qy      41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
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Qy      61 ProGlnGluValSerThrThrAspThrLysValIleGlyAsnGlySerPheGlyValVal 80
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Qy      81 TyrGlnAlaIysLeuCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp 100
Db      350 TATCAGCCAAACTTTGTGACTCAGAGAACTGGTGGCCATCAAGAAAGTTCTTCAGGAC 409
Qy      101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
Db      410 AAGCGATTAAAGAACCGAGAGCTCCAGATCATGAGAAAGTAGTACTGTAAACATAGTC 469
Qy      121 ArgLeuArgThrPhePheThrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
Db      470 CGATTCCGGTATTCTTCTACTCGAGTGGCGAGAAAGATGAGGTCTACCTTAACCTG 529
Qy      141 ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys 160

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Db      590 CAGACACTCCCTGTGTATCTATGTCAAGTTGTATATGTACAGCTGTTTCAAGAGTCTAGCC 649
Qy      181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuLeuAsp 200
Db      650 TATATCCATTCCTTTGGGATCTGCCATCGAGACATTAACACACAGAACCTCTTGTCTGGAT 709
Qy      201 ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly 220
Db      710 CCTGATACAGCTGTATTAACACTCTGCGACTTTTGGAAAGTGCAAGCAGCTGTCGAGGA 769
Qy      221 GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly 240
Db      770 GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCCACAGAGCTGATCTTTGGA 829
Qy      241 AlaThrAspTyrThrSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu 260
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Db      1010 TTCAAATTCCTCCCAATCAAGGCACATCTTGTGACGAAGTCTTTCGGCCCCGAATCTCA 1069
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Db      1070 CCAGAGGCAATCGCACTGTGTAGCCGTCTCTCGAGTACACGCCGACCCCGCTTAACA 1129
Qy      341 ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProhenValLysHis 360
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Db      1190 CCAAAATGGCGGAGACACACTGCTCCCTCTTCAACTTTTACCACCTCAAGAACTGTCAAGTAA 1249
Qy      381 ProProLeuAlaThrIleLeuIleProProHisAlaArgile 394
Db      1250 CCACCTCTGGCCACCACCATCTCTTATCCCTCTCAGCTCGGATT 1291

RESULT 8
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LOCUS      AR097211 1972 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6071694.
ACCESSION AR097211
VERSION    AR097211.1 GI:12805941
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1972)
AUTHORS    Takashima,A., Hoshino,T., Imahori,K., Saito,K.-i., Shiratsuchi,A.
TITLE      Screening method for therapeutic agents against Alzheimer's disease
            and Sato,S.
JOURNAL    Patent: US 6071694-A 2 06-JUN-2000;
FEATURES   Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      1.75e-183 Length:      1972

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Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: 2 Gaps: 1

US-10-733-816-2 (1-394) x AR097211 (1-1972)

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QY 41 AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg 60
DB 230 GATTAAGATGGCAGCAGGTTAACACAGTGGTGGCACTCTTGACAGAGGTCTTGACAGG 289
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QY 161 GlnThrLeuProValLileTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla 180
DB 590 CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTACAGCTGTTCAGAGTCTAGCC 649
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DB 650 TATATCCATTCTTTGGGATCTGCCATCGAGACATTAACACACAGAACCTCTTGCTGGAT 709
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DB 1010 TTCAAAATTCGCCAAATCAAGGCACATCTCTTGGACGAAGTCTTTGGGCCCCCACTCCA 1069
QY 321 ProGluAlaLileAlaLeuCysSerArgLeuGluTyrThrProThrAlaArgLeuThr 340
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QY 341 ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis 360
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QY 381 ProProLeuAlaThrLileLeuLileProProHisAlaArgLile 394
DB 1250 CCACCTCTGGCCACCATCTTAATCCCTCTCAGCTCGGATT 1291

RESULT 9
LOCUS BD181611 1972 bp DNA linear PAT 15-MAY-2003
DEFINITION Method of the phosphorylation of tau protein.
ACCESSION BD181611
VERSION BD181611.1 GI:30792529
KEYWORDS JP 2002335983-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1972)
AUTHORS Ishiguro,K., Sato,S., Uchida,Y. and Imahori,K.
TITLE Method of the phosphorylation of tau protein
JOURNAL Patent: JP 2002335983-A 1 26-NOV-2002;
MITSUBISHI CHEMICAL CORP
COMMENT OS Rattus sp. (rat)
PN JP 2002335983-A/1
PD 26-NOV-2002
PF 30-APR-2002 JP 2002129146
PI KOICHI ISHIGURO, SHOBU SATO, YO UCHIDA, KAZUTOMO IMAHORI PC
C12N15/09,C12P21/02//C12N9/12,C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
CC Method of the phosphorylation of tau protein
FH Key Location/Qualifiers
FT source 1..1932
FT /organism='Rattus sp. (rat)'
FT /organism='Rattus sp.'
FT /mol_type='genomic DNA'
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ORIGIN

Alignment Scores:
Pred. No.: 1.75e-183 Length: 1972
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: 2 Gaps: 1

US-10-733-816-2 (1-394) x BD181611 (1-1972)

QY 7 GluGlyGlyGly-----MetSerGlyArgProArgThrThrSerPhe 20
DB 110 GAAGGAAAAGGTGAATCGAGAGAGCCATCATGTGCGGGCGACCGAGAACCCACCTCCTTT 169
QY 21 AlaGluSerCysLysProValGlnProSerAlaPheGlySerMetLysValSerArg 40
DB 170 GCGGAGAGTGCAGGACGAGCTTCAAGCTTTGGTAGCATGAAGATGATAGCA 229
QY 41 AspLysAspGlySerLysValThrThrValValAlaThrProGlyGlnGlyProAspArg 60
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QY 101 LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal 120
DB 410 AAGCGATTTAAGAACCCAGAGAGCTCCAGATCATGAGAAAGCTAGACTCACTTAACATAGTC 469
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QY 181 TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp 200
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DB 830 GCCACCGATTACACGCTAGTAGATGATGTCTGTCAGCGCTGTGTGTTGGCTGAATTG 889
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DB 1070 CCAGAGCAATCGACTGTGTAGCGTCTCTGAGGTACAGCGGACCGCCCGCGCTTAACA 1129
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DB 1250 CCACCTTGCGCCACCATCTTATCTCTTCTCCCTCCTCAGCTCGGATT 1291

RESULT 10
E08007
LOCUS E08007 1972 bp RNA linear PAT 29-SEP-1997
DEFINITION DNA encoding tau protein kinase I.
ACCESSION E08007

VERSION E08007.1 GI:2176138
KEYWORDS JP 1994239893-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1972)
AUTHORS Ishiguro, K., Sato, N., Uchida, I. and Imahori, K.
TITLE PHOSPHORYLATION OF TAU PROTEIN
JOURNAL Patent: JP 1994239893-A 1 30-AUG-1994;
MITSUBISHI KASEI CORP
COMMENT OS Rattus sp. (rat)
PN JP 1994239893-A/1
PD 30-AUG-1994
PF 03-JUL-1992 JP 1992177241
PI OSHIGURO KOICHI, SATO NAOTAKE, UCHIDA ISAO, IMAHORI KAZUTOMO
PC C07K13/00, C12Q1/48//A61K37/56;
CC strandedness: Double;
CC topology: Linear;
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Db 1250 CCACCTTCGCGCACCATCTCTTATCCCTCTCACGCTCGGATT 1291

RESULT 11
BC060743
LOCUS
DEFINITION
Mus musculus glycogen synthase kinase 3 beta, mRNA (CDNA clone
MGC:68385 IMAGE:4022374), complete cds.
ACCESSION
BC060743
VERSION
BC060743.1 GI:38511427
KEYWORDS
MGC.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2841)
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., DeJong, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Hutchins, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Sapich, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Abrahamson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Small, D.E.,
Schneringer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2841)
Strausberg, R.
Direct Submission
Submitted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-ehgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 120 Row: h Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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/tissue_type="Mammary tumor metastasized to lung.
MMTV-LTR/Mnt1 model. Expression driven by an MMTV-LTR
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Qy	341	ProLeuGluAlaCySAlaHisSerPhePheAspGluLeuArgAspProAsnValIyeHis	360
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Qy	361	ProAsnGlyArgAspThrProAlaLeuPheAsnPhethrThrGlnGluLeuSerSerAsn	380
Db	2503	CCAAATGGGGGAGACACACCTGCCTCTTCAACTTTTACCACTCAAGAACTGTCAAGTAAC	2562
Qy	381	ProProLeuAlaThrIleLeuLeuProHisAlaArgIle	394
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LOCUS			
DEFINITION		8304 bp mRNA linear ROD 15-JAN-2005	
ACCESSION		Mus musculus mRNA for glycogen synthase kinase 3 beta/tau protein	
VERSION		kinase 1, complete cds.	
KEYWORDS		AB066114	
SOURCE		AB066114.1 GI:57834171	
ORGANISM		Mus musculus (house mouse)	
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		Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
REFERENCE		1	
AUTHORS		Sano Y., Nakano, A., Hirai, K., Ohta, S., Yanagisawa, M., Sato, S. and	
		Inahori, K.	
TITLE		Glycogen synthase kinase 3b gene: complete genomic and cDNA	
JOURNAL		structures	
REFERENCE		2 (bases 1 to 8304)	
AUTHORS		Sano, Y.	
TITLE		Direct Submission	
JOURNAL		Submitted (13-JUL-2001) Yumiko Sano, National Institute of Advanced	
		Industrial Science and Technology (AIST), Research Center for	
		Glycoscience (RCG), Glycogene Function Team; Central-2 OSL, 1-1-1	
		Umezono, Tsukuba, Ibaraki, 305-8568, Japan	
		(E-mail: yumiko.sano@aist.go.jp, Tel: 81-29-861-3197,	
		Fax: 81-29-861-3191)	
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Percent Similarity: 98.0%      Conservative: 0
Best Local Similarity: 98.0%      Mismatches: 2
Query Match:      96.8%      Indels:      6
DB:              6          Gaps:      1

US-10-733-816-2 (1-394) x AB066114 (1-8304)

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Qy      121 ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu 140
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Qy      301 PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro 320
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RESULT 13
AX821914 LOCUS 1231 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 42 from Patent WO03068961.
ACCESSION AX821914
VERSION AX821914.1 GI:39725135
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
AUTHORS Andrews,P.A., Walsh,J.A. and Gokhale,P.A.
TITLE Method to modify differentiation of pluripotential stem cells
JOURNAL Patent: WO 03068961-A 42 21-AUG-2003;
Axordia Limited (GB)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
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Score:          2013.00      Matches:      383
Percent Similarity: 99.7%      Conservative: 0
Best Local Similarity: 99.7%      Mismatches: 1
Query Match:      96.7%      Indels:      0
DB:              2          Gaps:      0

US-10-733-816-2 (1-394) x AX821914 (1-1231)

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RESULT 14

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LOCUS

DEFINITION

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Sequence 6 from Patent WO03000882.

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AX701656
VERSION AX701656.1 GI:29537197
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS Holder, J.C.
TITLE Transgenic models for glucose homeostasis comprising human gsk-3
JOURNAL Patent: WO 0300882-A 6 03-JAN-2003;
SMITHKLINE BEECHAM PLC (GB)
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Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 1..52e-183 Length: 1263
Score: 2013.00 Matches: 383
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 96.7% Indels: 0
DB: 2 Gaps: 0

US-10-733-816-2 (1-394) x AX701656 (1-1263)

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RESULT 15

CR536510

LOCUS

DEFINITION

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ACCESSION

CR536510.1 GI:49168505

VERSION

Full ORF shuttle clone, Gateway(TM), complete cds.

KEYWORDS

Full ORF shuttle clone, Gateway(TM), complete cds.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 1263)

Halleck A., Ebert, L., Mkundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)

Unpublished

2 (bases 1 to 1263)

Halleck A., Ebert, L., Mkundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Direct Submission

Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

TITLE

JOURNAL

REFERENCE

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Qy 91 LeuValAlaIleLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIle 110

Contact: Inge Ariant
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics and RZPD.

This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. .AAAAA GCA GGC TCC ACC (ARG).

The stopcodon is followed by the 3' att site:
(stop)GACCCAGCTTCTT. att Compared to the reference sequence
BC012760

We did not find any amino acid exchanges.

Clone distribution: http://www.rzpd.de/products/orfclones/.

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 1.52e-183 Length: 1263
Score: 2013.00 Matches: 383
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 96.7% Indels: 0
DB: 5 Gaps: 0

US-10-733-816-2 (1-394) x CR536510 (1-1263)

Qy 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2006, 17:25:11 ; Search time 34 Seconds
(without alignments)
818.678 Million cell updates/sec

Title: US-10-733-816-2

Perfect score: 2081

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Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	1919	92.2	387	7	US-11-299-324-18
7	1883.5	90.5	361	6	US-10-733-816-3
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42	1246	59.9	409	7	US-11-056-3558-33900	Sequence 33900, A
43	1246	59.9	409	7	US-11-056-3558-77778	Sequence 77778, A
44	1246	59.9	409	7	US-11-056-3558-100020	Sequence 100020, A
45	1246	59.9	409	7	US-11-056-3558-111259	Sequence 111259, A

ALIGNMENTS

RESULT 1

US-10-733-816-2
; Sequence 2, Application US/10733816
; Publication No. US2006008932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Seiby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-2

Query Match 100.0%; Score 2081; DB 6; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.3e-122;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEYMPMEGGMSGRPTTSF	AECKPVQPSAFGSMKVRDQSGSKVTTVVATPGQ3PDR	60
Db	1	MEYMPMEGGMSGRPTTSF	AECKPVQPSAFGSMKVRDQSGSKVTTVVATPGQ3PDR	60
QY	61	PQVSYTDTKVI	NGSFGVYVYQAKL	120
Db	61	PQVSYTDTKVI	NGSFGVYVYQAKL	120
QY	121	RLBYFFYSSEKDE	VYLNVLDPETVYRVARHYSRAKOTLPVIVKLYMQLFSLA	180
Db	121	RLBYFFYSSEKDE	VYLNVLDPETVYRVARHYSRAKOTLPVIVKLYMQLFSLA	180
QY	181	YIHSFGICHRDI	KPQNLLDPDTAVLKLCDPFGSAKQLVRGPNVSYICSYRAPELIFG	240
Db	181	YIHSFGICHRDI	KPQNLLDPDTAVLKLCDPFGSAKQLVRGPNVSYICSYRAPELIFG	240

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QY 241 ADYTSIDVWSAGCVLAELLLQPIPPGDSGVDQLVEIKVLGTTRQIREMNPNTY 300
Db 241 ADYTSIDVWSAGCVLAELLLQPIPPGDSGVDQLVEIKVLGTTRQIREMNPNTY 300
QY 301 FKFPQIKAHPTWKVFRPTTPEALACSLRLVETPTARLTPLACAHSPFDELDPNVKH 360
Db 301 FKFPQIKAHPTWKVFRPTTPEALACSLRLVETPTARLTPLACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394

RESULT 2
US-10-733-816-1
; Sequence 1, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCES: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-1

Query Match 97.3%; Score 2024; DB 6; Length 420;
Best Local Similarity 100.0%; Pred. No. 8.5e-119; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0;

QY 11 MSGRPRTTSPAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTK 70
Db 1 MSGRPRTTSPAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTK 60
QY 71 VIONGSGVVYQAKLDCSGBELVAIKKVLQDKRPFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VIONGSGVVYQAKLDCSGBELVAIKKVLQDKRPFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
QY 131 EKDEVLNLVLDYVPETVVRVYARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSPGICHR 190
Db 121 EKDEVLNLVLDYVPETVVRVYARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSPGICHR 180
QY 191 DIKPNLLDPTAVLKLCDFGSAKQLV RGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIKPNLLDPTAVLKLCDFGSAKQLV RGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLLQPIPPGDSGVDQLVEIKVLGTTRQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLLQPIPPGDSGVDQLVEIKVLGTTRQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPTTPEALACSLRLVETPTARLTPLACAHSPFDELDPNVKHNGRDTPALF 370
Db 301 WTKVFRPTTPEALACSLRLVETPTARLTPLACAHSPFDELDPNVKHNGRDTPALF 360

RESULT 4
US-11-299-324-15
; Sequence 15, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
```

```
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
US-11-299-324-10
; Sequence 10, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-299-324-10

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-118; Indels 0; Gaps 0;
Matches 383; Conservative 0; Mismatches 1;

QY 11 MSGRPRTTSPAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTK 70
Db 1 MSGRPRTTSPAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTK 60
QY 71 VIONGSGVVYQAKLDCSGBELVAIKKVLQDKRPFKNRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VIONGSGVVYQAKLDCSGBELVAIKKVLQDKRPFKNRELQIMRKLDHCNIVRLRYFFYSSG 120
QY 131 EKDEVLNLVLDYVPETVVRVYARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSPGICHR 190
Db 121 EKDEVLNLVLDYVPETVVRVYARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSPGICHR 180
QY 191 DIKPNLLDPTAVLKLCDFGSAKQLV RGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIKPNLLDPTAVLKLCDFGSAKQLV RGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLLQPIPPGDSGVDQLVEIKVLGTTRQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLLQPIPPGDSGVDQLVEIKVLGTTRQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPTTPEALACSLRLVETPTARLTPLACAHSPFDELDPNVKHNGRDTPALF 370
Db 301 WTKVFRPTTPEALACSLRLVETPTARLTPLACAHSPFDELDPNVKHNGRDTPALF 360

RESULT 4
US-11-299-324-15
; Sequence 15, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
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LENGTH: 433
TYPE: PRT
ORGANISM: Homo sapiens
US-11-299-324-15

Query Match
Best Local Similarity 95.9%; Score 1996.5; DB 7; Length 433;
Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

11 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 70
1 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 60
71 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 130
61 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 120
131 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 190
121 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 180
191 DIKPQNLLDPTAVLKLDCFGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
181 DIKPQNLLDPTAVLKLDCFGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
251 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTFEKFPQIKAH 310
241 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTFEKFPQIKAH 300
311 WTK-----VFRPRTTPEAIALCSRLLEYTPTARLTPLACAHSPFDELDPN 357
301 WTKDSSGTGHTSGVRFRTTPEAIALCSRLLEYTPTARLTPLACAHSPFDELDPN 360
358 VHKPNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
361 VKLPNGRDTPALNFTTQELSSNPPLATILIPPHARI 397

RESULT 6
US-11-299-324-18
Sequence 18, Application US/11299324
Publication No. US20060127388A1
GENERAL INFORMATION:
APPLICANT: Cain, Michael
TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
FILE REFERENCE: WYE-052
CURRENT APPLICATION NUMBER: US/11/299,324
CURRENT FILING DATE: 2005-12-09
PRIOR APPLICATION NUMBER: US 60/634,813
PRIOR FILING DATE: 2004-12-10
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent in version 3.3
SEQ ID NO 18
LENGTH: 387
TYPE: PRT
ORGANISM: Homo sapiens
US-11-299-324-18

Query Match 92.2%; Score 1919; DB 7; Length 387;
Best Local Similarity 98.6%; Pred. No. 2.6e-112; Indels 0; Gaps 0;
Matches 364; Conservative 3; Mismatches 2;

11 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 70
1 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 60
71 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 130
61 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 120
131 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 190
121 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 180
191 DIKPQNLLDPTAVLKLDCFGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
181 DIKPQNLLDPTAVLKLDCFGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
251 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTFEKFPQIKAH 310
241 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTFEKFPQIKAH 300
311 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLACAHSPFDELDPNPKNGRDTPALF 370
301 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLACAHSPFDELDPNPKNGRDTPALF 360
371 NFFTQELSS 379
361 NFFTQDANT 369

LENGTH: 433
TYPE: PRT
ORGANISM: Homo sapiens
US-11-299-324-15

Query Match
Best Local Similarity 95.9%; Score 1996.5; DB 7; Length 433;
Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

11 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 70
1 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 60
71 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 130
61 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 120
131 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 190
121 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 180
191 DIKPQNLLDPTAVLKLDCFGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
181 DIKPQNLLDPTAVLKLDCFGSAKQVLRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
251 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTFEKFPQIKAH 310
241 WSAGCVLAELLGQPIFGDSGVQDLVEIKVLGTPTREQIREMNPNTFEKFPQIKAH 300
311 WTK-----VFRPRTTPEAIALCSRLLEYTPTARLTPLACAHSPFDELDPN 357
301 WTKDSSGTGHTSGVRFRTTPEAIALCSRLLEYTPTARLTPLACAHSPFDELDPN 360
358 VHKPNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
361 VKLPNGRDTPALNFTTQELSSNPPLATILIPPHARI 397

RESULT 5
US-11-283-329-216
Sequence 216, Application US/11283329
Publication No. US20060134670A1
GENERAL INFORMATION:
APPLICANT: Piu, Fabrice
TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
HORMONE NUCLEAR RECEPTORS
FILE REFERENCE: ACADIA 043A
CURRENT APPLICATION NUMBER: US/11/283,329
CURRENT FILING DATE: 2005-11-18
PRIOR APPLICATION NUMBER: 60/629,811
PRIOR FILING DATE: 2004-11-19
NUMBER OF SEQ ID NOS: 242
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 216
LENGTH: 433
TYPE: PRT
ORGANISM: Homo sapiens
US-11-283-329-216

Query Match
Best Local Similarity 95.9%; Score 1996.5; DB 7; Length 433;
Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

11 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 70
1 MSGRPRTTTSAESCKPVQPSAFGSMKVSRLDQSGSKVTTTVAATPGQGPDRPQEVSYDTK 60
71 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 130
61 VINGSGFVVYQAKLDCSSELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYSSG 120
131 EKKDEVILNLVLDYVPETVVRVARHYSRAKQTLPIVIVKLYMQLFRSLAYIHSFGICHR 190

```
RESULT 7
US-10-733-816-3
; Sequence 3, Application US/10733816
; Publication No. US2006008932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733.816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211.412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-3

Query Match      90.5%; Score 1883.5; DB 6; Length 361;
Best Local Similarity 91.6%; Pred. No. 3.9e-110;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 MEYMPGGGMSGRPTTSFAESCKPVQPSAFGSMKVSRDKQSKVTTVATPGQGPDR 60
DB 1 MEYMPGGG-----GSKVTTVATPGQGPDR 27
QY 61 PQSVSYTDTKVIENGSGVYVYQAKLDCSGLVAIKKVLQDKRPNRELOIMRKLDHCNIV 120
DB 28 PQSVSYTDTKVIENGSGVYVYQAKLDCSGLVAIKKVLQDKRPNRELOIMRKLDHCNIV 87
QY 121 RLRYFFYSSEKKEDEVYLNLDVYVETVYVARHYSRKQTLPIVYVKLYMYQLFRSLA 180
DB 88 RLRYFFYSSEKKEDEVYLNLDVYVETVYVARHYSRKQTLPIVYVKLYMYQLFRSLA 147
QY 181 YIHSFGICHRDIKPNLLDPDTAVLKCDFGSAKQLVRGEPNVSYICSYRYRAPELIFG 240
DB 148 YIHSFGICHRDIKPNLLDPDTAVLKCDFGSAKQLVRGEPNVSYICSYRYRAPELIFG 207
QY 241 ATDYTSIDVWSAGCVLAELLGQPIPPGDSGVDQVEIIVKVLGTPTRQIREMNNPYTE 300
DB 208 ATDYTSIDVWSAGCVLAELLGQPIPPGDSGVDQVEIIVKVLGTPTRQIREMNNPYTE 267
QY 301 FKPPQIKAHPTWKVFRPTTPEALCSRLLEYTPARLTPLACAHSAFFDELDPNVKH 360
DB 268 FKPPQIKAHPTWKVFRPTTPEALCSRLLEYTPARLTPLACAHSAFFDELDPNVKH 327
QY 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
DB 328 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 361

RESULT 8
US-11-299-324-16
; Sequence 16, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variants of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09

; PRIOR APPLICATION NUMBER: US 60/634,813
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-299-324-16

Query Match      86.9%; Score 1808; DB 7; Length 388;
Best Local Similarity 91.4%; Pred. No. 2.1e-105;
Matches 351; Conservative 0; Mismatches 1; Indels 32; Gaps 1;

QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSRDKQSKVTTVATPGQGPDRPQSVSYTDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSRDKQSKVTTVATPGQGPDRPQSVSYTDTK 60
QY 71 VIENGSGVYVYQAKLDCSGLVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFVSSG 130
DB 61 VIENGSGVYVYQAKLDCSGLVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFVSSG 120
QY 131 EKKDEVYLNLDVYVETVYVARHYSRKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKKDEVYLNLDVYVETVYVARHYSRKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPNLLDPDTAVLKCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 250
DB 181 DIKPNLLDPDTAVLKCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVDQVEIIVKVLGTPTRQIREMNNPYTEFKPPQIKAH 310
DB 241 WSAGCVLAELLGQPIPPGDSGVDQVEIIVKVLGTPTRQIREMNNPYTEFKPPQIKAH 270
QY 311 WTKVFRPTTPEALCSRLLEYTPARLTPLACAHSAFFDELDPNVKHPNGRDTPALF 370
DB 271 --KVPFRPTTPEALCSRLLEYTPARLTPLACAHSAFFDELDPNVKHPNGRDTPALF 328
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 329 NFTTQELSSNPPLATILIPPHARI 352

RESULT 9
US-10-733-816-5
; Sequence 5, Application US/10733816
; Publication No. US2006008932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733.816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211.412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-5

Query Match      77.3%; Score 1609; DB 6; Length 447;
```

Best Local Similarity 80.6%; Pred. No. 5.6e-93;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;
QY 8 GGGMSGRPRT-TSFAESCKPVQPSAFSGSMKVRDQKGVKVTWATPGQPPRPOEVS 66
Db 73 GGGSGGPGAGTSFPPP-----GVKLG--DSGKVTTVATLGGQPPERSQEVAY 119
QY 67 TDTKVIKNGSGFVVYQAKLDCSGLVAIKKVLQDKFKRELQIMRKLCHNCNIVRLRYFF 126
Db 120 TDIKVIKNGSGFVVYQARLAETRELVAIKKVLQDKFKRELQIMRKLCHNCNIVRLRYFF 179
QY 127 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 186
Db 180 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 239
QY 187 ICHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIFGATDYS 299
QY 247 SIDWSAGCVLAELLGQPIFGDGSVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFGDGSVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 359
QY 307 KAHPTWKVFRPRTPPPAIALCSLLLETTPTARLTPLEACAHSPFDELRODENVKHPNGRDT 366
Db 360 KAHPTWKVFRPRTPPPAIALCSLLLETTPTARLTPLEACAHSPFDELRODENVKHPNGRDT 419
QY 367 PALFNFTTQBLSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIOPSLNAILIPPHLR 446

RESULT 10

US-10-733-816-4

; Sequence 4, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-4

Query Match 77.3%; Score 1609; DB 6; Length 483;

Best Local Similarity 80.6%; Pred. No. 6e-93;

Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPRT-TSFAESCKPVQPSAFSGSMKVRDQKGVKVTWATPGQPPRPOEVS 66
Db 73 GGGSGGPGAGTSFPPP-----GVKLG--DSGKVTTVATLGGQPPERSQEVAY 119
QY 67 TDTKVIKNGSGFVVYQAKLDCSGLVAIKKVLQDKFKRELQIMRKLCHNCNIVRLRYFF 126
Db 120 TDIKVIKNGSGFVVYQARLAETRELVAIKKVLQDKFKRELQIMRKLCHNCNIVRLRYFF 179

QY 127 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 186
Db 180 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 239
QY 187 ICHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIFGATDYS 299
QY 247 SIDWSAGCVLAELLGQPIFGDGSVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFGDGSVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 359
QY 307 KAHPTWKVFRPRTPPPAIALCSLLLETTPTARLTPLEACAHSPFDELRODENVKHPNGRDT 366
Db 360 KAHPTWKVFRPRTPPPAIALCSLLLETTPTARLTPLEACAHSPFDELRODENVKHPNGRDT 419
QY 367 PALFNFTTQBLSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIOPSLNAILIPPHLR 446

RESULT 11

US-10-553-520-85

; Sequence 85, Application US/105535320
; Publication No. US20060188885A1
; GENERAL INFORMATION:
; APPLICANT: Bodian, Dale
; APPLICANT: Daouti, Sherif
; APPLICANT: Kumar, Chandrika
; APPLICANT: Latario, Brian
; APPLICANT: Quintavalla, Joseph
; TITLE OF INVENTION: High throughput functional genomic
; TITLE OF INVENTION: screening methods for osteoarthritis
; FILE REFERENCE: 4-33178
; CURRENT APPLICATION NUMBER: US/10/553,520
; PRIOR APPLICATION NUMBER: 60/463,933
; PRIOR FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 483
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-553-520-85

Query Match 77.3%; Score 1609; DB 6; Length 483;

Best Local Similarity 80.6%; Pred. No. 6e-93;

Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPRT-TSFAESCKPVQPSAFSGSMKVRDQKGVKVTWATPGQPPRPOEVS 66
Db 73 GGGSGGPGAGTSFPPP-----GVKLG--DSGKVTTVATLGGQPPERSQEVAY 119
QY 67 TDTKVIKNGSGFVVYQAKLDCSGLVAIKKVLQDKFKRELQIMRKLCHNCNIVRLRYFF 126
Db 120 TDIKVIKNGSGFVVYQARLAETRELVAIKKVLQDKFKRELQIMRKLCHNCNIVRLRYFF 179
QY 127 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 186
Db 180 YSSGEKKDEVLYNLVDYPTVTVRVARHYSRAKQTLPIVYKLYMYQLFRSLAYIHSFG 239
QY 187 ICHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLLDPPDTAVLKLCDFGSAKQVRGEPNVSYICSRYYRAPELIFGATDYS 299
QY 247 SIDWSAGCVLAELLGQPIFGDGSVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFGDGSVDQVLEIKVLGTPTREQIREMNPNTYEFKPPQI 359
QY 307 KAHPTWKVFRPRTPPPAIALCSLLLETTPTARLTPLEACAHSPFDELRODENVKHPNGRDT 366
Db 360 KAHPTWKVFRPRTPPPAIALCSLLLETTPTARLTPLEACAHSPFDELRODENVKHPNGRDT 419

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QY 367 PALFNFTQELSSNPPLATILIPPHAR 393
Db 420 PPLENFSAGELSIQPSLNAILIPPHLR 446

RESULT 12
US-10-733-816-7
; Sequence 7, Application US/10733816
; Publication No. US2006008932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-7

Query Match 76.3%; Score 1588; DB 6; Length 351;
Best Local Similarity 86.2%; Pred. No. 8.8e-92;
Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 46 KVTTVATPGQDRPQEVSYTDTKVIGNSFGVYQAKLDSGELVAIKKVLQDKRFKN 105
Db 3 KVTTVATLGGPERSQEVAYTDIKVIGNSFGVYQARLAETRELVAIKKVLQDKRFKN 62

QY 106 RELQIMRKLDHCNIVRLRYFFYSSEKDEVLNLDVYVETVYRVARHYSRAKOTLPV 165
Db 63 RELQIMRKLDHCNIVRLRYFFYSSEKDEVLNLDVYVETVYRVARHFTKAKTIPI 122

QY 166 IYVKLYMYQLFRSLAYTHSFGICHRDIKPNQLLLDPTAVLKLCDFGSAKQLVRGPNVS 225
Db 123 LYVKVYMYQLFRSLAYTHSFGVCHRDIKPNQLLLVDPDTAVLKLCDFGSAKQLVRGPNVS 182

QY 226 YICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLGQPIFFGDSGVQDLVEIIVLGT 285
Db 183 YICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLGQPIFFGDSGVQDLVEIIVLGT 242

QY 286 PTREQIREMNPNTPEKFPQIKAHPTWKVFRPTTPEALCSRLLEYTPTARLTPLEAC 345
Db 243 PTREQIREMNPNTPEKFPQIKAHPTWKVFRPTTPEALCSRLLEYTPTSSRLSPLAC 302

QY 346 AHSFFDELDRPNVKGPNRGRTDPAFNFTTQELSSNPPLATILIPPHAR 393
Db 303 AHSFFDELRCGLTQLPNNRPLPLPPLNFSAGELSIOPSLNAILIPPHLR 350

RESULT 14
US-11-299-324-14
; Sequence 14, Application US/11299324
; Publication No. US20060127388A1
; GENERAL INFORMATION:
; APPLICANT: Cain, Michael
; APPLICANT: Yaworsky, Paul J
; TITLE OF INVENTION: Variance of Glycogen Synthase Kinase 3 and Uses Thereof
; FILE REFERENCE: WYE-052
; CURRENT APPLICATION NUMBER: US/11/299,324
; CURRENT FILING DATE: 2005-12-09
; PRIOR FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 14
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-299-324-14

Query Match 68.0%; Score 1416; DB 7; Length 278;
Best Local Similarity 100.0%; Pred. No. 3.4e-81;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 MSGRPRTTSPAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLDCSGBELVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGBELVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSYG 120
QY 131 EKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKKDEVYLNLDVYPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIRPQNLLDPDTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIRPQNLLDPDTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIKV 282
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIKV 272

Db 315 RTPPEAVDLVSRLLQVSPNLRSTAMEAIVHPFFDELDRDNTLPLNGRALPPLFNFKPQEL 374
QY 378 -SSNPPLATILIPPHAR 393
Db 375 KGASLELLSKLIPDHAR 391

Search completed: September 15, 2006, 17:28:44
Job time : 36 secs

RESULT 15
US-11-056-355B-82944
; Sequence 82944, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 82944
; LENGTH: 399
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(399)
; OTHER INFORMATION: Ceres Seq. ID no. 12668003
US-11-056-355B-82944

Query Match 61.7%; Score 1283; DB 7; Length 399;
Best Local Similarity 65.8%; Pred. No. 8.9e-73;
Matches 248; Conservative 49; Mismatches 66; Indels 14; Gaps 6;
QY 30 PSAFGSMKVSRRDK-----DGSKVTT---VWATPGQGPDRP-QEVSYTDTKVIGNSFG 78
Db 16 PEGINEMKIKDDKEMEAADVNGTGTGHIIVTTIGKNGQPKQTISYMAERIVGQGSFG 75
QY 79 VYQAKLDCSGBELVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSSEKKQDEVYL 138
Db 76 IVFOAKCLETGETVAIKKVLQDKRPNRELOIMRKLDHCNIVRLRYFFYSSEKKQDEVYL 134
QY 139 NLVLDVYPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHRDIKPNL 197
Db 135 NLVLEYPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHRDIKPNL 194
QY 198 LLDPDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVL 257
Db 195 LVNPHQHWKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVL 254
QY 258 AELLGQPIPPGDSGVDQVLEIKKVLGTPTRQIREMKNPNYTFKFPQIKAHPTWKVFRP 317
Db 255 AELLGQPLPPGSGVDQVLEIKKVLGTPTRQIREMKNPNYTFKFPQIKAHPTWKVFRP 314
QY 318 RTPPEALCSRLLPYTPPTARLTPLECAHSFPDELDRDNPVKNPGRDTPALFNFTTQEL 377
Db 315 RTPPEAVDLVSRLLQVSPNLRSTAMEAIVHPFFDELDRDNTLPLNGRALPPLFNFKPQEL 374

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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:24:21 ; Search time 183 Seconds
(without alignments)
997.304 Million cell updates/sec

Title: US-10-733-816-2

Perfect score: 2081

Sequence: 1 MEYMPMEGGMSGRPTTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2081	100.0	394	3	US-09-916-109-2
2	2081	100.0	394	4	US-10-211-412A-2
3	2081	100.0	394	5	US-10-689-461-2
4	2024	97.3	420	3	US-09-916-109-1
5	2024	97.3	420	4	US-10-211-412A-1
6	2024	97.3	420	4	US-10-278-759-7
7	2024	97.3	420	5	US-10-482-524-4
8	2024	97.3	420	5	US-10-772-636-72
9	2024	97.3	420	5	US-10-689-461-1
10	2024	97.3	420	5	US-10-840-060-257
11	2024	97.3	420	6	US-11-288-493-72
12	2013	96.7	414	4	US-10-746-545-31
13	2013	96.7	420	4	US-10-278-759-6
14	2013	96.7	420	4	US-10-135-255-1
15	2013	96.7	420	4	US-10-746-545-15
16	2013	96.6	420	4	US-10-746-545-18
17	2010	96.6	420	4	US-10-278-759-2
18	2010	96.6	420	4	US-10-322-153A-1
19	2010	96.6	420	4	US-10-613-728-8
20	1997	96.0	385	4	US-10-684-421-53
21	1997	96.0	385	5	US-10-941-635-53
22	1996.5	95.9	433	4	US-10-278-759-8
23	1996.5	95.9	433	4	US-10-278-759-14
24	1996.5	95.9	433	4	US-10-302-812-62
25	1996.5	95.9	433	4	US-10-408-765A-1360
26	1996.5	95.9	433	5	US-10-828-669-5
27	1996.5	95.9	433	5	US-10-770-726-65

28	1883.5	90.5	361	3	US-09-916-109-3	Sequence 3, Appli
29	1883.5	90.5	361	4	US-10-211-412A-3	Sequence 3, Appli
30	1883.5	90.5	361	5	US-10-689-461-3	Sequence 3, Appli
31	1877	90.2	367	4	US-10-746-545-32	Sequence 32, Appli
32	1872.5	90.0	361	4	US-10-450-422-1	Sequence 1, Appli
33	1817	87.3	352	4	US-10-664-421-31	Sequence 31, Appli
34	1817	87.3	352	4	US-10-746-545-16	Sequence 16, Appli
35	1817	87.3	352	4	US-10-746-545-17	Sequence 17, Appli
36	1817	87.3	352	5	US-10-941-635-31	Sequence 17, Appli
37	1817	87.3	352	6	US-11-021-951-167	Sequence 167, App
38	1803	86.6	350	4	US-10-746-545-27	Sequence 27, Appli
39	1666.5	80.1	407	5	US-10-732-923-1457	Sequence 1457, Ap
40	1834.5	78.5	428	5	US-10-491-467-13	Sequence 13, Appli
41	1609	77.3	447	3	US-09-916-109-5	Sequence 5, Appli
42	1609	77.3	447	4	US-10-211-412A-5	Sequence 5, Appli
43	1609	77.3	447	5	US-10-689-461-5	Sequence 4, Appli
44	1609	77.3	483	3	US-09-916-109-4	Sequence 4, Appli
45	1609	77.3	483	4	US-10-211-412A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-916-109-2

; Sequence 2, Application US/09916109

; Patent No. US20020082408A1

; GENERAL INFORMATION:

; APPLICANT: Harrison, Stephen D.

; APPLICANT: Hall, John A.

; APPLICANT: Calderon-Cacia, Maria

; APPLICANT: Zhong, Ziyang

; APPLICANT: Fang, Eric Y.

; APPLICANT: Coit, Doris G.

; APPLICANT: Nguyen, Steve H.

; APPLICANT: Medina-Selby, Angelica

; TITLE OF INVENTION: GSK3 POLYPEPTIDES

; FILE REFERENCE: PP-15876.002/200130.524

; CURRENT APPLICATION NUMBER: US/09/916,109

; CURRENT FILING DATE: 2001-07-25

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 394

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-916-109-2

Query Match 100.0%; Score 2081; DB 3; Length 394;

Best Local Similarity 100.0%; Pred. No. 3.7e-169;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEYMPMEGGMSGRPTTSFAESCKPVQOPSAGSMKVS	RDKGSKVTVVATPGQCPDR	60
Db	1	MEYMPMEGGMSGRPTTSFAESCKPVQOPSAGSMKVS	RDKGSKVTVVATPGQCPDR	60
Qy	61	PQEVSYTDTKVI	NGSGFVVYQAKL	CDSGELVAIKKVLQDKR
Db	61	PQEVSYTDTKVI	NGSGFVVYQAKL	CDSGELVAIKKVLQDKR
Qy	121	RLRYFFYSSEKKEDEV	LVNLVDVPTVTVRAHYSRAKQTL	PVIIVKLYMYQLF
Db	121	RLRYFFYSSEKKEDEV	LVNLVDVPTVTVRAHYSRAKQTL	PVIIVKLYMYQLF
Qy	181	YIHSFGICHRDI	KPNLLDPD	TAVALKCDFGSAKQLVRGEPNVS
Db	181	YIHSFGICHRDI	KPNLLDPD	TAVALKCDFGSAKQLVRGEPNVS
Qy	241	ATDTSSIDVWSAGCV	LAELLGQIP	PPGDSGDVQLVEI
Db	241	ATDTSSIDVWSAGCV	LAELLGQIP	PPGDSGDVQLVEI
Qy	301	FKFPQIKAHPTWK	VRPRTPEPE	IALCSRLLETPTTARLT
Db	301	FKFPQIKAHPTWK	VRPRTPEPE	IALCSRLLETPTTARLT

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Db 301 FKFPQKAHPWTKVFRPRTPEAIALCSRLLLEVTPTARLTPLACAHSPFDELDPNVKH 360
Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394

RESULT 2
US-10-211-412A-2
; Sequence 2, Application US/10211412A
; Publication No. US2003007798A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.004/200130.524D1
; CURRENT APPLICATION NUMBER: US/10/211.412A
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412A-2

Query Match 100.0%; Score 2081; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.7e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSBDKDGSKVTTVVATPGGQPD 60
Db 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSBDKDGSKVTTVVATPGGQPD 60
Qy 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIV 120
Db 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIV 120
Qy 121 RLRYFFYSGEKKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
Db 121 RLRYFFYSGEKKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
Qy 181 YHISFGICHRDIKPNLLDPTAVLKLCDPGSAKQIVRGEPNVSYICSRYRAPELIFG 240
Db 181 YHISFGICHRDIKPNLLDPTAVLKLCDPGSAKQIVRGEPNVSYICSRYRAPELIFG 240
Qy 241 ATDYSIDVWSAGCVLAELLGQPIFGSDGVDQVLEIIVKLGTPTRQIREMNPYTE 300
Db 241 ATDYSIDVWSAGCVLAELLGQPIFGSDGVDQVLEIIVKLGTPTRQIREMNPYTE 300
Qy 301 FKFPQKAHPWTKVFRPRTPEAIALCSRLLLEVTPTARLTPLACAHSPFDELDPNVKH 360
Db 301 FKFPQKAHPWTKVFRPRTPEAIALCSRLLLEVTPTARLTPLACAHSPFDELDPNVKH 360
Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394

RESULT 3
US-10-689-461-2
; Sequence 2, Application US/10689461
; Publication No. US20050048511A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
```

```
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/689,461
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-461-2

Query Match 100.0%; Score 2081; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.7e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSBDKDGSKVTTVVATPGGQPD 60
Db 1 MEYMPMEGGGMSGRPRTTSAESCKPVQPSAFGSMKVSBDKDGSKVTTVVATPGGQPD 60
Qy 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIV 120
Db 61 PQEVSYTDTKVINGSGFVGYQAKLDCSGELVAIKVLDQKRFKNRELQIMRKLDHCNIV 120
Qy 121 RLRYFFYSGEKKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
Db 121 RLRYFFYSGEKKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLA 180
Qy 181 YHISFGICHRDIKPNLLDPTAVLKLCDPGSAKQIVRGEPNVSYICSRYRAPELIFG 240
Db 181 YHISFGICHRDIKPNLLDPTAVLKLCDPGSAKQIVRGEPNVSYICSRYRAPELIFG 240
Qy 241 ATDYSIDVWSAGCVLAELLGQPIFGSDGVDQVLEIIVKLGTPTRQIREMNPYTE 300
Db 241 ATDYSIDVWSAGCVLAELLGQPIFGSDGVDQVLEIIVKLGTPTRQIREMNPYTE 300
Qy 301 FKFPQKAHPWTKVFRPRTPEAIALCSRLLLEVTPTARLTPLACAHSPFDELDPNVKH 360
Db 301 FKFPQKAHPWTKVFRPRTPEAIALCSRLLLEVTPTARLTPLACAHSPFDELDPNVKH 360
Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394

RESULT 4
US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. US20020082408A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-1

Query Match      97.3%; Score 2024; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCKPVQQPSPAFGSMKVSVDKDGSKVTTTVAATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTTFAESCKPVQQPSPAFGSMKVSVDKDGSKVTTTVAATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCDSELVAIKKVLQDKRFPKRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCDSELVAIKKVLQDKRFPKRELOIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSVICSRYRPAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSVICSRYRPAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPRTTPEAIALCSRLLLEYPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTTPEAIALCSRLLLEYPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412A-1
; Sequence 1, Application US/10211412A
; Publication No. US2003007798A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.004/2001130.524D1
; CURRENT APPLICATION NUMBER: US/10/211.412A
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412A-1

Query Match      97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCKPVQQPSPAFGSMKVSVDKDGSKVTTTVAATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTTFAESCKPVQQPSPAFGSMKVSVDKDGSKVTTTVAATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCDSELVAIKKVLQDKRFPKRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCDSELVAIKKVLQDKRFPKRELOIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSVICSRYRPAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSVICSRYRPAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPRTTPEAIALCSRLLLEYPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTTPEAIALCSRLLLEYPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 6
US-10-278-759-7
; Sequence 7, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237.70020.US
; CURRENT APPLICATION NUMBER: US/10/278.759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-278-759-7

Query Match      97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCKPVQQPSPAFGSMKVSVDKDGSKVTTTVAATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTTFAESCKPVQQPSPAFGSMKVSVDKDGSKVTTTVAATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCDSELVAIKKVLQDKRFPKRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCDSELVAIKKVLQDKRFPKRELOIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSVICSRYRPAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPTAVLKLCDFGSAKOLVRGEPNVSVICSRYRPAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTREQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPRTTPEAIALCSRLLLEYPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTTPEAIALCSRLLLEYPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360
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Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384
RESULT 7
US-10-482-524-4
; Sequence 4, Application US/10482524
; Publication No. US20040261137A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham PLC
; APPLICANT: Holder, Julie C
; TITLE OF INVENTION: Models for Metabolic Disorders
; FILE REFERENCE: PG4458
; CURRENT APPLICATION NUMBER: US/10/482,524
; CURRENT FILING DATE: 2003-12-22
; PRIOR FILING DATE: 2001-06-26
; PRIOR FILING DATE: 2002-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-524-4

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQPSVSTDTK 70
Db 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQPSVSTDTK 60
QY 71 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 120
QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLDDPDTAVLKLDCFGSAKQLVRGEPNVVICSRYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLDDPDTAVLKLDCFGSAKQLVRGEPNVVICSRYRAPELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLQGPFPFGSGVDQLVEIIVKLGTPTREQIREMNPNTYTFKFPQKAHP 310
Db 241 WSAGCVLAELLQGPFPFGSGVDQLVEIIVKLGTPTREQIREMNPNTYTFKFPQKAHP 300
QY 311 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 370
Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 360
RESULT 8
US-10-772-636-72
; Sequence 72, Application US/10772636
; Publication No. US20050042687A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; FILE REFERENCE: MPI03-015PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/772,636
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/510,351
; PRIOR FILING DATE: 2003-10-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-772-636-72

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQPSVSTDTK 70
Db 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGGQDPQPSVSTDTK 60
QY 71 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 120
QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPLVYVVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLDDPDTAVLKLDCFGSAKQLVRGEPNVVICSRYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLDDPDTAVLKLDCFGSAKQLVRGEPNVVICSRYRAPELIFGATDYTSSIDV 240
QY 251 WSAGCVLAELLQGPFPFGSGVDQLVEIIVKLGTPTREQIREMNPNTYTFKFPQKAHP 310
Db 241 WSAGCVLAELLQGPFPFGSGVDQLVEIIVKLGTPTREQIREMNPNTYTFKFPQKAHP 300
QY 311 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 370
Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDRDNNVKNPGRDTPALF 360
RESULT 9
US-10-689-461-1

; Sequence 1, Application US/10689461
; Publication No. US2005004851A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/689,461
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-689-461-1

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCCKPVQPSAFGSMKVS RDKGSKVTTVATPGQGPDRPQSVSYTDTK 70
Db 1 MSGRPRTTTFAESCCKPVQPSAFGSMKVS RDKGSKVTTVATPGQGPDRPQSVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCSGLVAIKVQLQDKRPNRELQIMRKLDHCNI VRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGLVAIKVQLQDKRPNRELQIMRKLDHCNI VRLRYFFYSYG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPVYVVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPVYVVKLYMQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLCAHSPFDELDRDNPVKNHNGRDTPALF 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLCAHSPFDELDRDNPVKNHNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 10
US-10-840-060-257
; Sequence 257, Application US/10840060
; Publication No. US20050227243A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited
; APPLICANT: Deak, Peter
; APPLICANT: Frenz, Lisa
; APPLICANT: Glover, David
; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: 10069/2012
; CURRENT APPLICATION NUMBER: US/10/840,060

; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: PCT/GB02/04780
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 0126506.5
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: GB 0128384.5
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: GB 0203185.4
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 257
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-840-060-257

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 3e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCCKPVQPSAFGSMKVS RDKGSKVTTVATPGQGPDRPQSVSYTDTK 70
Db 1 MSGRPRTTTFAESCCKPVQPSAFGSMKVS RDKGSKVTTVATPGQGPDRPQSVSYTDTK 60

QY 71 VINGSGFVVYQAKLDCSGLVAIKVQLQDKRPNRELQIMRKLDHCNI VRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGLVAIKVQLQDKRPNRELQIMRKLDHCNI VRLRYFFYSYG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPVYVVKLYMQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPVYVVKLYMQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPTAVLKLCDFGSAKQVLRGEPNVSYCSRYRPAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLCAHSPFDELDRDNPVKNHNGRDTPALF 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLCAHSPFDELDRDNPVKNHNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 11
US-11-288-493-72
; Sequence 72, Application US/11288493
; Publication No. US20060078947A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 22584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MPI03-015PIRNONMIN
; CURRENT APPLICATION NUMBER: US/11/288,493
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US/10/772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05

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; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-288-493-72

Query Match
Best Local Similarity 97.3%; Score 2024; DB 6; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTSAESCKPVQQPSAFSGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTK 70
DB 1 MSGRPRTTSAESCKPVQQPSAFSGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYDTK 60
QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLLDPDTAVLKCDPFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 250
DB 181 DIKPQNLLDPDTAVLKCDPFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQKAHP 310
DB 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQKAHP 300
QY 311 WTKVFRPRTPEAIACSLRLEYYTPARLTPLECAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEAIACSLRLEYYTPARLTPLECAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 12
US-10-746-545-31
; Sequence 31, Application US/10746545
; Publication No. US20040171075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphera Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L
; APPLICANT: Pettilo, Peter A
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Patent in version 3.2
; SEQ ID NO 31
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-746-545-31

Query Match
Best Local Similarity 96.7%; Score 2013; DB 4; Length 414;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLLDPDTAVLKCDPFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 250
DB 181 DIKPQNLLDPDTAVLKCDPFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQKAHP 310
DB 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIREMNPNTYEFKFPQKAHP 300
QY 311 WTKVFRPRTPEAIACSLRLEYYTPARLTPLECAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEAIACSLRLEYYTPARLTPLECAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 13
US-10-278-759-6
; Sequence 6, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237.70020.US
; CURRENT APPLICATION NUMBER: US/10/278,759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-278-759-6

Query Match
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Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 1, Application US/10135255
; Publication No. US2003012532A1
; GENERAL INFORMATION:
; APPLICANT: TER HAAR, ERNST
; APPLICANT: SWENSON, LOVORKA
; APPLICANT: GREEN, JEREMY
; APPLICANT: ARNOST, MICHAEL J.
; TITLE OF INVENTION: INHIBITORS OF GSK-3 AND CRYSTAL STRUCTURES OF GSK-3B
; TITLE OF INVENTION: PROTEIN AND PROTEIN COMPLEXES
; FILE REFERENCE: VPI/01-02
; CURRENT APPLICATION NUMBER: US/10/135,255
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/361,899
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/297,094
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/287,366
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-255-1

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Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLHDCNIVRLRYFFYS 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLHDCNIVRLRYFFYS 120
QY 131 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPNLLDPPDPAVLKCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 250
DB 181 DIKPNLLDPPDPAVLKCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQIKAH 310
DB 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPTPEAIAICSRLLVPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEAIAICSRLLVPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

Search completed: September 15, 2006, 17:28.05
Job time : 185 secs

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QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384
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US-10-746-545-15
; Sequence 15, Application US/10746545
; Publication No. US20040171075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphra Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L
; APPLICANT: Pettilo, Peter A
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 15
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-746-545-15

Query Match 96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.6e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MSGRPTTSFAESCKPVQPSAFSGSMKVSDDKSGKVTTVVATPGQDPDRPQEVSYDTK 60
QY 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLHDCNIVRLRYFFYS 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLHDCNIVRLRYFFYS 120
QY 131 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVYLNLDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKPNLLDPPDPAVLKCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 250
DB 181 DIKPNLLDPPDPAVLKCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 240
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DB 301 WTKVFRPTPEAIAICSRLLVPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:12:25 ; Search time 51 Seconds
 (without alignments)
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Title: US-10-733-816-2

Perfect score: 2081

Sequence: 1 MEYMPGCGMSGRPRTTSF.....QELSSNPPLATILIPPHARI 394

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2024	97.3	420	2	US-09-336-038-1
4	2024	97.3	420	2	US-09-916-109-1
5	2024	97.3	420	2	US-10-211-412B-1
6	2024	97.3	420	2	US-09-538-092-1163
7	2010	96.6	420	1	US-08-602-264A-14
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9	1883.5	90.5	361	2	US-10-211-412B-3
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11	1609	77.3	447	2	US-10-211-412B-5
12	1609	77.3	483	2	US-09-916-109-4
13	1609	77.3	483	2	US-10-211-412B-4
14	1609	77.3	483	2	US-09-538-092-1162
15	1588	76.3	351	2	US-09-916-109-7
16	1588	76.3	351	2	US-10-211-412B-7
17	1588	76.3	387	2	US-09-916-109-6
18	1588	76.3	387	2	US-10-211-412B-6
19	1256	60.4	412	2	US-09-347-801-21
20	1256	60.4	412	2	US-09-854-731-21
21	1242	59.7	410	2	US-09-347-801-10
22	1242	59.7	410	2	US-09-854-731-10
23	1240	59.6	402	2	US-09-347-801-16
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25	1232	59.2	405	2	US-09-347-801-20
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27	1232	59.2	407	2	US-09-347-801-23	Sequence 23, Appl
28	1232	59.2	407	2	US-09-854-731-23	Sequence 23, Appl
29	1226	58.9	411	2	US-09-347-801-22	Sequence 22, Appl
30	1226	58.9	411	2	US-09-854-731-22	Sequence 22, Appl
31	1165.5	56.0	399	2	US-09-347-801-14	Sequence 14, Appl
32	1165.5	56.0	399	2	US-09-854-731-14	Sequence 14, Appl
33	1001.5	48.1	395	2	US-09-248-796A-18499	Sequence 18499, A
34	940	45.2	370	2	US-09-538-092-623	Sequence 623, App
35	674	32.4	411	2	US-09-248-796A-18500	Sequence 18500, A
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37	483.5	23.2	649	2	US-09-949-016-10147	Sequence 10147, A
38	478.5	23.0	334	2	US-09-949-016-10777	Sequence 10777, A
39	476.5	22.9	379	2	US-09-411-628-14	Sequence 14, Appl
40	476.5	22.9	379	2	US-10-174-794-14	Sequence 14, Appl
41	476.5	22.9	379	2	US-09-538-092-1021	Sequence 1021, Ap
42	472.5	22.7	379	2	US-08-622-277A-8	Sequence 8, Appl
43	472.5	22.7	379	2	US-09-025-580-25	Sequence 25, Appl
44	472.5	22.7	379	2	US-09-642-749-25	Sequence 25, Appl
45	472.5	22.7	631	2	US-09-417-197-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1

US-09-916-109-2
 ; Sequence 2, Application US/09916109
 ; Patent No. 6465231
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrison, Stephen D.
 ; APPLICANT: Hall, John A.
 ; APPLICANT: Calderon-Cacia, Maria
 ; APPLICANT: Zhong, Ziyang
 ; APPLICANT: Fang, Eric Y.
 ; APPLICANT: Colt, Dotis G.
 ; APPLICANT: Nguyen, Steve H.
 ; APPLICANT: Medina-Selby, Angelica
 ; TITLE OF INVENTION: GSK3 POLYPEPTIDES
 ; FILE REFERENCE: PP-15876.002/200130.524
 ; CURRENT APPLICATION NUMBER: US/09/916,109
 ; CURRENT FILING DATE: 2001-07-25
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 394
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-916-109-2

Query Match	Score	DB 2;	Length	394;
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Indels	0;	Gaps	0;	
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Qy	61	POEVSYTDTKVINGSGFVYVQAKLDCSGELVAIKKVLQDKRFKNRELIQMRKLDHCNIV	120	
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Qy	121	RLRYFFYSSEKKEDEVYLNVLVDYVPTVTVRVARHYSRAKQTLPVIVVKLYMYQLFRSLA	180	
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Qy	181	YIHSFGICHRDIPQNLLDPDPAVLKCDFGSAKQLVRGEPNVSYICSRVYRAPELIFG	240	
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Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
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RESULT 2
US-10-211-412B-2
; Sequence 2, Application US/10211412B
; Patent No. 671624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211.412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-2

Query Match 100.0%; Score 2081; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.1e-221;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 YHSGFICHRIKPNLLDPTAVLKCDPFGSAKQLVGEPNVSYICSYRYRAPELIFG 240
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Qy 301 FKPPQIKAHPTKVFRTPTPEAIALCSRLLEYTPTARLTPLECAHSFFDELDPNVKH 360
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Qy 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALNFTTQELSSNPPLATILIPPHARI 394

RESULT 3
US-09-336-038-1
; Sequence 1, Application US/093336038
; Patent No. 6417185
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; GENERAL INFORMATION:
; APPLICANT: Goff, Dane
; APPLICANT: Harrison, Steven
; APPLICANT: Nuss, John
; APPLICANT: Ring, David B.
; APPLICANT: Zhou, Xiaohui A.
; TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
; FILE REFERENCE: 1443.003
; CURRENT APPLICATION NUMBER: US/09/336.038
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/089,978
; EARLIER FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-038-1

Query Match 97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.9e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VINGSGFVVYQAKLDCSGLVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYS 120

Qy 131 EKDEVYLVNVLVDYVPETVYVARHYSRAKOTLPVIYVKLYMYQLFRSLAYIHSFGICHR 190
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Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4
US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916.109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 420
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US-09-916-109-1

Query Match
Best Local Similarity 97.3%; Score 2024; DB 2; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYDTDK 60

Qy 71 VINGSGFVVYQAKLDCDSELVAIKKVLQDRFKNRELQIMRKLDHCNIIVRLRYFFSYSSG 130
Db 61 VINGSGFVVYQAKLDCDSELVAIKKVLQDRFKNRELQIMRKLDHCNIIVRLRYFFSYSSG 120

Qy 131 EKDEVTYLNLDVYVPTVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVTYLNLDVYVPTVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNLLDPTAVLKLCDGSAKQLVRGEPNVSICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNLLDPTAVLKLCDGSAKQLVRGEPNVSICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLLGGPIPPGSDGVQDLVEIHKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLLGGPIPPGSDGVQDLVEIHKVLGTPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTTPEALCALCSRLEVTPTARLTPLLECAHSFFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCALCSRLEVTPTARLTPLLECAHSFFDELDPNVKHPNGRDTPALF 360

Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412B-1
; Sequence 1, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Medina-Selby, Angelica
; APPLICANT: Nguyen, Steve H.
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211.412B
; PRIOR FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2002-07-31
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-1

Query Match
Best Local Similarity 97.3%; Score 2024; DB 2; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYDTDK 60

Qy 71 VINGSGFVVYQAKLDCDSELVAIKKVLQDRFKNRELQIMRKLDHCNIIVRLRYFFSYSSG 130
Db 61 VINGSGFVVYQAKLDCDSELVAIKKVLQDRFKNRELQIMRKLDHCNIIVRLRYFFSYSSG 120

Qy 131 EKDEVTYLNLDVYVPTVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVTYLNLDVYVPTVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNLLDPTAVLKLCDGSAKQLVRGEPNVSICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNLLDPTAVLKLCDGSAKQLVRGEPNVSICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLLGGPIPPGSDGVQDLVEIHKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLLGGPIPPGSDGVQDLVEIHKVLGTPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPTTPEALCALCSRLEVTPTARLTPLLECAHSFFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCALCSRLEVTPTARLTPLLECAHSFFDELDPNVKHPNGRDTPALF 360

Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 6
US-09-538-092-1163
; Sequence 1163, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1163
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P49841
US-09-538-092-1163

Query Match
Best Local Similarity 97.3%; Score 2024; DB 2; Length 420;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPTTSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVVATPGQGPDRPQEVSYDTDK 60

Qy 71 VINGSGFVVYQAKLDCDSELVAIKKVLQDRFKNRELQIMRKLDHCNIIVRLRYFFSYSSG 130
Db 61 VINGSGFVVYQAKLDCDSELVAIKKVLQDRFKNRELQIMRKLDHCNIIVRLRYFFSYSSG 120

Qy 131 EKDEVTYLNLDVYVPTVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVTYLNLDVYVPTVYVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKPNLLDPTAVLKLCDGSAKQLVRGEPNVSICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNLLDPTAVLKLCDGSAKQLVRGEPNVSICSYRYRAPELIFGATDVTSSIDV 240

Qy 251 WSAGCVLAELLLGGPIPPGSDGVQDLVEIHKVLGTPTREQIREMNPNTYEFKFPQIKAH 310

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Db 241 WSAGCVLAELLGQPIFGDSGVQDLVRIIKVLGTTTREQIREMNPNTYTFKPPQIKAHF 300
QY 311 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 7
US-08-602-264A-14
; Sequence 14, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; ORIGINAL SOURCE:
; ORGANISM: human being
US-08-602-264A-14

Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 2.56-213;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSORPRTTFAESCKPVPQPSAFSGSMKVS RDKGSKVTTVATPGGQDPQPSVYTDTK 70
Db 1 MSORPRTTFAESCKPVPQPSAFSGSMKVS RDKGSKVTTVATPGGQDPQPSVYTDIK 60
QY 71 VIGNSGFVVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKLDHCNIVRLRYFFSSG 130
Db 61 LIGNSGFVVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKLDHCNIVRLRYFFSSG 120
QY 131 EKDEYVNLNLDVVPETVYVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 190

Db 121 EKDEYVNLNLDVVPETVYVARHYSRAKQTLPIVYVVKLYMQLFRSLAYIHSFGICHR 180
QY 191 DIKPQNLLDDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIPGATDYTSSIDV 250
Db 181 DIKPQNLLDDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIPGATDYTSSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSGVQDLVRIIKVLGTTTREQIREMNPNTYTFKPPQIKAHF 310
Db 241 WSAGCVLAELLGQPIFGDSGVQDLVRIIKVLGTTTREQIREMNPNTYTFKPPQIKAHF 300
QY 311 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 8
US-09-916-109-3
; Sequence 3, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.9e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 MEYMPMEGGGMSGRPTTTSFAESCKPVPQPSAFSGSMKVS RDKGSKVTTVATPGGQDP 60
Db 1 MEYMPMEGGG-----GSKVTTTVATPGGQDP 27
QY 61 POEVSYTDTKVIGNGSFGVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKLDHCNIV 120
Db 28 POEVSYTDTKVIGNGSFGVYQAKLSDSGELVAIKVLDKRPKNRELQIMRKLDHCNIV 87
QY 121 RLRYFFYSSEKKEDEVYLNLDVVPETVYVARHYSRAKQTLPIVYVVKLYMQLFRSLA 180
Db 88 RLRYFFYSSEKKEDEVYLNLDVVPETVYVARHYSRAKQTLPIVYVVKLYMQLFRSLA 147
QY 181 YIHSFGICHRDIKPNLLDDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFG 240
Db 148 YIHSFGICHRDIKPNLLDDPTAVLKLCDGSAKQLVRGEPNVSYICSRYYRAPELIFG 207
QY 241 ATDYTSSIDVWSAGCVLAELLGQPIFGDSGVQDLVRIIKVLGTTTREQIREMNPNTY 300
Db 208 ATDYTSSIDVWSAGCVLAELLGQPIFGDSGVQDLVRIIKVLGTTTREQIREMNPNTY 267
QY 301 FKPPQIKAHFWTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKH 360
Db 268 FKPPQIKAHFWTKVFRPRTTPEAIALCSRLLEYTPTARLTPLEACAHSPFDELDPNVKH 327

QY 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 361

RESULT 9

US-10-211-412B-3
; Sequence 3, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.9e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 MEYMPMEGGMSGRPTTSFAESCKPVQPSAFSGSMKVRSDKSGKVTTVATPGQGPDR 60
Db 1 MEYMPMEGGG-----GSKVTTTVATPGQGPDR 27
QY 61 POEVSYTDTKVINGSGFVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIV 120
Db 28 POEVSYTDTKVINGSGFVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIV 87
QY 121 RLRYFFYSSEKKEDEVYLNLDVYPETVYVARHYSRKQTLPLVIYVKLYMYQLFRSLA 180
Db 88 RLRYFFYSSEKKEDEVYLNLDVYPETVYVARHYSRKQTLPLVIYVKLYMYQLFRSLA 147
QY 181 YIHSFGICHRDIKPNLLDPPDTAVLKLDCFGSAKQLVGEPNVSYICSYRRAPELIFG 240
Db 148 YIHSFGICHRDIKPNLLDPPDTAVLKLDCFGSAKQLVGEPNVSYICSYRRAPELIFG 207
QY 241 ADYTSIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIIREMNNYTE 300
Db 208 ADYTSIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIIREMNNYTE 267
QY 301 FKPPQIKAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKH 360
Db 268 FKPPQIKAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKH 327
QY 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 361

RESULT 10

US-09-916-109-5
; Sequence 5, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria

; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-5

Query Match 77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6.7e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GGGMSGRPR-TSFAESCKPVQPSAFSGSMKVRSDKSGKVTTVATPGQGPDRPOEVS 66
Db 73 GGGSGGPGAGTSFPPP-----GVKLGK--DSGKVTTVATLGGPERSQEVAY 119
QY 67 TDTKVIINGSGFVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIVRLRYFF 126
Db 120 TDTKVIINGSGFVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIVRLRYFF 179
QY 127 YSSGKKEDEVYLNLDVYPETVYVARHYSRKQTLPLVIYVKLYMYQLFRSLAYIHSFG 186
Db 180 YSSGKKEDEVYLNLDVYPETVYVARHYSRKQTLPLVIYVKLYMYQLFRSLAYIHSFG 239
QY 187 ICHRDIKPNLLDPPDTAVLKLDCFGSAKQLVGEPNVSYICSYRRAPELIFGATDYS 246
Db 240 VCHRDIKPNLLDPPDTAVLKLDCFGSAKQLVGEPNVSYICSYRRAPELIFGATDYS 299
QY 247 SIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIIREMNNYTEFKPPQI 306
Db 300 SIDVWSAGCVLAELLGQPIFGDSGVDQVLEIKVLGTPTRQIIREMNNYTEFKPPQI 359
QY 307 KAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKHGRDT 366
Db 360 KAHPTWKVFRPRTPPEAIALCSRLLEYTPTARLTPLACAHSPFDELDRDNPVKHGRDT 419
QY 367 PALFNFETTSQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFESAGELSIQPSLNAILIPPHLR 446

RESULT 11

US-10-211-412B-5
; Sequence 5, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 447

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/ TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-5

Query Match      77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6.7e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GCGMGRPRT-TSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVATPGGPRPQEVSY 66
Db 73 GCGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119
QY 67 TDTKVIENGSGFVVYQAKLDCSGELVAIKKVLQDKFKFKRELQIMRKLDHCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQARLAETRELVAIKKVLQDKFKFKRELQIMRKLDHCNIVRLRYFF 179
QY 127 YSSGEKKDEVILNLVDYVPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYTHSPG 186
Db 180 YSSGEKKDELYNLVLEYVYPETVYRVARHFTKAKLTIPILYVKVYMYQLFRSLAYTHSQG 239
QY 187 ICHRDIKPQNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS 246
Db 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS 299
QY 247 SIDWSAGCVLAELLGQPIFFGDSGVDQLVEIKVLGTPTRQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFFGDSGVDQLVEIKVLGTPTRQIREMNPNTYEFKPPQI 359
QY 307 KAHPTWTKVFRPTPPAIALCSRLLEYTPTARLTPLCAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHPTWTKVFKSRTPPAIALCSLLLEYTPTSSRLSPLEACAHSPFDELCLGTQLPNNRPL 419
QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAILIPPHLR 446

RESULT 12
US-09-916-109-4
; Sequence 4, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-4

Query Match      77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 7.6e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GCGMGRPRT-TSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVATPGGPRPQEVSY 66
Db 73 GCGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119
QY 67 TDTKVIENGSGFVVYQAKLDCSGELVAIKKVLQDKFKFKRELQIMRKLDHCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQARLAETRELVAIKKVLQDKFKFKRELQIMRKLDHCNIVRLRYFF 179
QY 127 YSSGEKKDEVILNLVDYVPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYTHSPG 186
Db 180 YSSGEKKDELYNLVLEYVYPETVYRVARHFTKAKLTIPILYVKVYMYQLFRSLAYTHSQG 239
QY 187 ICHRDIKPQNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS 246
Db 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS 299
QY 247 SIDWSAGCVLAELLGQPIFFGDSGVDQLVEIKVLGTPTRQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFFGDSGVDQLVEIKVLGTPTRQIREMNPNTYEFKPPQI 359
QY 307 KAHPTWTKVFRPTPPAIALCSRLLEYTPTARLTPLCAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHPTWTKVFKSRTPPAIALCSLLLEYTPTSSRLSPLEACAHSPFDELCLGTQLPNNRPL 419
QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAILIPPHLR 446

RESULT 13
US-10-211-412B-4
; Sequence 4, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-4

Query Match      77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 7.6e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GCGMGRPRT-TSFAESCKPVQPSAFGSMKVSRRDKGSKVTTVATPGGPRPQEVSY 66
Db 73 GCGSGGPGAGTSFPPP-----GVKLR--DSGKVTTVATLGGPERSQEVAY 119
QY 67 TDTKVIENGSGFVVYQAKLDCSGELVAIKKVLQDKFKFKRELQIMRKLDHCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQARLAETRELVAIKKVLQDKFKFKRELQIMRKLDHCNIVRLRYFF 179
QY 127 YSSGEKKDEVILNLVDYVPETVYRVARHYSRAKQTLPIYVVKLYMYQLFRSLAYTHSPG 186
Db 180 YSSGEKKDELYNLVLEYVYPETVYRVARHFTKAKLTIPILYVKVYMYQLFRSLAYTHSQG 239
QY 187 ICHRDIKPQNLLDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS 246
Db 240 VCHRDIKPQNLLVDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTS 299
QY 247 SIDWSAGCVLAELLGQPIFFGDSGVDQLVEIKVLGTPTRQIREMNPNTYEFKPPQI 306
Db 300 SIDWSAGCVLAELLGQPIFFGDSGVDQLVEIKVLGTPTRQIREMNPNTYEFKPPQI 359
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QY 307 KAHPTWKVFRPRTTPEAIALCSRLLEYTPVARTPLEACAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHPTWKVFRSRTTPEAIALCSRLLEYTPSSRLSPLEACAHSPFDELRCGLTQLPNNRPL 419
QY 367 PALFNTTQELSNPPLATILIPPHAR 393
Db 420 PPLNFNSAGELSIOQSLNAILIPPHLR 446

RESULT 14

US-09-538-092-1162
; Sequence 1162, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqFormat Version 0.9
; SEQ ID NO 1162
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P49840
US-09-538-092-1162

Query Match 77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 7.6e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

QY 8 GCGMSGRPRT-TSFAISCKPVQPSAFSGSKVSRDKGSKVTTVATPGQGRDPRQEVSY 66
Db 73 GGGSGGPGAGTSFPPP-----GVKLR--DSGKVTWVATLGQGPERSQEVAY 119
QY 67 TDTKTVNGSGFVYVQAKLDSGELVAIKVLDQKRFKRELOIMRKLDHCNIVRLRYFF 126
Db 120 TDKTVNGSGFVYVQARLAETRELVAIKVLDQKRFKRELOIMRKLDHCNIVRLRYFF 179
QY 127 YSSGKKDEYVNLVLDYVPVTVRVARHYSRAKQTLPIYVYVQVLFPSRLAYIHSFG 186
Db 180 YSSGKKDEYVNLVLDYVPVTVRVARHFTKAKLTIPILYVYVQVLFPSRLAYIHSQ 239
QY 187 ICHRDIKPQNLDDPDTAVLKLCDFGSAKOLVRGENSVYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIKPQNLDDPDTAVLKLCDFGSAKOLVRGENSVYICSRYYRAPELIFGATDYS 299
QY 247 SIDVWSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQI 306
Db 300 SIDVWSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQI 359
QY 307 KAHPTWKVFRPRTTPEAIALCSRLLEYTPVARTPLEACAHSPFDELDPNVKHPNGRDT 366
Db 360 KAHPTWKVFRSRTTPEAIALCSRLLEYTPSSRLSPLEACAHSPFDELRCGLTQLPNNRPL 419
QY 367 PALFNTTQELSNPPLATILIPPHAR 393
Db 420 PPLNFNSAGELSIOQSLNAILIPPHLR 446

RESULT 15

US-09-916-109-7
; Sequence 7, Application US/09916109
; Patent No. 6465231

; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calgeron-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Coit, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876, 002/200130, 524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-916-109-7

Query Match 76.3%; Score 1588; DB 2; Length 351;
Best Local Similarity 86.2%; Pred. No. 9.5e-167;
Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

QY 46 KVTTVATPGQGRDPRQEVSYTDKTVIGNSFGVYVQAKLDSGELVAIKVLDQKRFKN 105
Db 3 KVTTVATLGQGPERSQEVAYTDKTVIGNSFGVYVQARLAETRELVAIKVLDQKRFKN 62
QY 106 RELOIMRKLDHCNIVRLRYFFYSSGKKDEYVNLVLDYVPVTVRVARHYSRAKQTLPV 165
Db 63 RELOIMRKLDHCNIVRLRYFFYSSGKKDEYVNLVLDYVPVTVRVARHFTKAKLTPI 122
QY 166 IYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLDDPDTAVLKLCDFGSAKOLVRGENSV 225
Db 123 LYVKLYMYQLFRSLAYIHSQGVCHRDIKPQNLDDPDTAVLKLCDFGSAKOLVRGENSV 182
QY 226 YICSRYYRAPELIFGATDYSIDVWSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLG 285
Db 183 YICSRYYRAPELIFGATDYSIDVWSAGCVLAELLGQPIFGDSDGVQDLVEIIVKLG 242
QY 286 PTREQIREMNPNTYEFKFPQIKAHPTWKVFRPRTTPEAIALCSRLLEYTPVARTPLEAC 345
Db 243 PTREQIREMNPNTYEFKFPQIKAHPTWKVFRSRTTPEAIALCSRLLEYTPSSRLSPLEAC 302
QY 346 AHSFFDELDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR 393
Db 303 AHSFFDELRCGLTQLPNNRPLPPLNFNSAGELSIOQSLNAILIPPHLR 350

Search completed: September 15, 2006, 17:13:51
Job time : 52 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:04:00 ; Search time 302 Seconds
(without alignments)
1206.808 Million cell updates/sec

Title: US-10-733-816-2
Perfect score: 2081
Sequence: 1 MEYMPMEGGMGSRPTTSP.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2013	96.7	420	1 GSK3B_HUMAN	P49841 homo sapien
2	2013	96.7	420	1 GSK3B_MOUSE	Q9wv60 mus musculus
3	2013	96.7	420	2 G6F127_HUMAN	Q6fi27 homo sapien
4	2013	96.7	420	2 Q5KU03_MOUSE	Q5ku03 m glycogen
5	2010	96.6	420	1 GSK3B_RAT	P18266 rattus norv
6	2006	96.4	420	2 Q5YJC2_SPECI	Q5yjc2 spermophilu
7	1959	94.1	421	2 Q9IBD2_BRARE	Q9ibd2 brachydanio
8	1959	94.1	421	2 Q9YH60_BRARE	Q9yh60 brachydanio
9	1931	92.8	420	2 Q91757_XENLA	Q91757 xenopus lae
10	1923	92.4	420	2 Q91627_XENLA	Q91627 xenopus lae
11	1793.5	86.2	496	2 Q4S0H0_TETNG	Q4s0h0 tetraodon n
12	1704.5	81.9	440	2 Q9YH61_BRARE	Q9yh61 brachydanio
13	1669.5	80.2	435	2 Q9IBD3_BRARE	Q9ibd3 brachydanio
14	1666.5	80.1	407	2 Q9NL43_CIOIN	Q9nl43 ciona intes
15	1632	78.4	414	2 Q61UG5_LYTVA	Q61ug5 lytechinus
16	1614	77.6	414	2 Q46150_PARLI	Q46150 paracentrot
17	1609	77.3	483	1 GSK3A_HUMAN	P49840 homo sapien
18	1607	77.2	483	1 GSK3A_RAT	P18265 rattus norv
19	1606	77.2	399	2 Q4SSG6_TETNG	Q4ssg6 tetraodon n
20	1594	76.6	388	2 Q68D16_HUMAN	Q68d16 homo sapien
21	1565	75.2	363	2 Q7QA46_ANOGA	Q7qa46 anopheles g
22	1542.5	74.1	1067	1 SGG_DROME	P18431 drosophila
23	1495.5	71.9	443	2 Q4H118_SUBDO	Q4h118 suberites d
24	1485	71.4	442	2 Q9GTK0_HYDAT	Q9gtk0 hydra atten
25	1443	69.3	431	2 Q58952_DUGJA	Q58952 dugesia jap
26	1343.5	64.6	362	2 Q9YOC2_CABEL	Q9yoc2 caenorhabdi
27	1342.5	64.5	362	2 Q9U2Q9_CABEL	Q9u2q9 caenorhabdi
28	1341.5	64.5	359	2 Q5WNK0_CAEBR	Q5wnk0 caenorhabdi
29	1305.5	62.7	501	1 GSK3H_DROME	P83101 drosophila
30	1302	62.6	402	2 Q4PH53_USTWA	Q4ph53 ustulago ma
31	1296	62.3	409	2 Q40886_PETHY	Q40886 petunia hyb

32	1294	62.2	423	2 Q6VM07_PHYPA	Q6vm07 physcomitre
33	1289.5	62.0	398	2 Q55X64_CRYNE	Q55x64 cryptococcu
34	1289.5	62.0	398	2 Q5KMR8_CRYNE	Q5kmr8 cryptococcu
35	1283	61.7	410	1 KSG5_ARATH	Q8vzd5 arabidopsis
36	1275.5	61.3	471	2 Q24139_TOBAC	Q24139 nicotiana t
37	1273.5	61.2	424	2 Q6VM11_PHYPA	Q6vm11 physcomitre
38	1273.5	61.2	471	2 Q82029_TOBAC	Q82029 nicotiana t
39	1273	61.2	401	2 Q6EUS4_ORYSA	Q6eus4 oryza sativ
40	1271	61.1	423	2 Q6VM08_PHYPA	Q6vm08 physcomitre
41	1269	61.0	412	2 Q4WDL1_ASPPU	Q4wdl1 aspergillus
42	1264	60.7	394	2 Q5AYX2_EMENI	Q5ayx2 aspergillus
43	1263.5	60.7	424	2 Q6AVQ3_ORYSA	Q6avq3 oryza sativ
44	1262.5	60.7	470	2 Q82038_PETHV	Q82038 petunia hyb
45	1262	60.6	355	2 Q6VM10_PHYPA	Q6vm10 physcomitre

ALIGNMENTS

RESULT 1
ID GSK3B_HUMAN STANDARD; PRT; 420 AA.
AC P49841; Q9BWH3; Q9UL47;
DT 01-OCT-1996, integrated into UniprotKB/Swiss-Prot.
DT 02-MAY-2002, sequence version 2.
DT 07-MAR-2006, entry version 70.
DE Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta).
GN Name=GSK3B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=95071278; PubMed=7980435;
RA Stambolic V., Woodgett J.R.;
RT "Mitogen inactivation of glycogen synthase kinase-3 beta in intact
RT cells via serine 9 phosphorylation.";
RL Biochem. J. 303:701-704(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Eye, and Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 185-202.
RX MEDLINE=99455114; PubMed=10523816; DOI=10.1038/sj.mp.4000538;
RA Rhoads A.R., Karkera J.D., Detera-Wadleigh S.D.;
RT "Radiation hybrid mapping of genes in the lithium-sensitive wnt
RT signaling pathway.";
RL Mol. Psychiatry 4:437-442(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-28.

RX MEDLINE=99417672; PubMed=10486203; DOI=10.1006/geno.1999.5875;
 RA Lau K.F., Miller C.C.J., Anderton B.H., Shaw P.C.;
 RT "Molecular cloning and characterization of the human glycogen synthase
 RL kinase-3beta promoter";
 RN Genomics 60:121-128(1999).
 RP CHARACTERIZATION.
 RX MEDLINE=98409636; PubMed=9736715; DOI=10.1073/pnas.95.19.11211;
 RA Delcomenne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;
 RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen
 RL synthase kinase 3 and protein kinase B/AKT by the integrin-linked
 RP kinase";
 RN Proc. Natl. Acad. Sci. U.S.A. 95:11211-11216(1998).
 RP INTERACTION WITH NIN.
 RX MEDLINE=20461863; PubMed=11004522; DOI=10.1016/S0167-4781(00)00127-5;
 RA Hong Y.-R., Chen C.-H., Chang J.-H., Wang S.-K., Sy W.-D., Chou C.-K.,
 RL Hwang S.-L.;
 RT "Cloning and characterization of a novel human ninein protein that
 RL interacts with the glycogen synthase kinase 3beta";
 RN Biochim. Biophys. Acta 1492:513-516(2000).
 RP PHOSPHORYLATION SITE THR-390.
 RX PubMed=15302935; DOI=10.1073/pnas.0404720101;
 RA Baulelell S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
 RL Li J., Cohn M.A., Cantley L.C., Gygi S.P.;
 RT "Large-scale characterization of HeLa cell nuclear phosphoproteins";
 RN Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).
 RP CHARACTERIZATION WITH GSK3B.
 RX PubMed=15752768; DOI=10.1016/j.bbrc.2005.02.089;
 RA Hou H.-C., Lee Y.-L., Cheng T.-S., Howng S.-L., Chang L.-K., Lu P.-J.,
 RL Hong Y.-R.;
 RT "Characterization of two non-testis-specific CABYR variants that bind
 RL to GSK3beta with a proline-rich extensin-like domain";
 RN Biochem. Biophys. Res. Commun. 329:1108-1117(2005).
 RP PHOSPHORYLATION SITE TYR-216, AND MASS SPECTROMETRY.
 RX PubMed=15592455; DOI=10.1038/nbt1046;
 RA Rush J., Moxitt A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
 RL Zha X.-M., Polakiewicz R.D., Comb M.J.;
 RT "Immunofluorescence profiling of tyrosine phosphorylation in cancer
 RL cells";
 RN Nat. Biotechnol. 23:94-101(2005).
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 35-386.
 RX MEDLINE=21334149; PubMed=11440715; DOI=10.1016/S0092-8674(01)00374-9;
 RA DeJani R., Fraser E., Roe S.M., Young N., Good V., Dale T.C.,
 RL Pearl L.H.;
 RT "Crystal structure of glycogen synthase kinase 3 beta: structural
 RL basis for phosphate-primed substrate specificity and autoinhibition";
 RN Cell 105:721-732(2001).
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 27-393 OF PHOSPHORYLATED
 RX MEDLINE=21605727; PubMed=11738041; DOI=10.1016/S0969-2126(01)00679-7;
 RA Bax B., Carter P.S., Lewis C., Guy A.R., Bridges A., Tanner R.,
 RL Pattman G., Mannix C., Culbert A.A., Brown M.J.B., Smith D.G.,
 RP Reith A.D.;
 RT "The structure of phosphorylated GSK-3beta complexed with a peptide,
 RL FRATtide, that inhibits beta-catenin phosphorylation";
 RN Structure 9:1143-1152(2001).
 RP -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
 CC the hormonal control of several regulatory proteins including
 CC glycogen synthase, MYB and the transcription factor JUN.
 CC Phosphorylates JUN at sites proximal to its DNA-binding domain,
 CC thereby reducing its affinity for DNA.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- ENZYME REGULATION: Inhibited when phosphorylated by AKT1.
 CC -1- SUBUNIT: Monomer (By similarity). Interacts with NIN and CABYR.
 CC -1- INTERACTION:
 CC Q7Z6N3:UPF3A; NDEXP=1; IntAct=EBI-373586, EBI-372587;
 CC -1- ALTERNATIVE PRODUCTS:
 CC

CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoIds=P49841-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49841-2; Sequence=VSP_004790;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Expressed in testis, thymus, prostate and
 CC ovary and weakly expressed in lung, brain and kidney.
 CC -1- PTM: Phosphorylated by AKT1 and ILK1.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
 CC subfamily.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC ENBL; L33801; AAA66475.1; -; mRNA.
 CC ENBL; BC000251; AAH00251.1; -; mRNA.
 CC ENBL; BC012760; AAH12760.1; -; mRNA.
 CC ENBL; AF098789; AAC69340.1; -; Genomic_DNA.
 CC ENBL; AF074333; AAD48517.1; -; Genomic_DNA.
 CC PIR; S53324; S53324.
 CC PDB; 1GNG; X-ray; A/B=27-393.
 CC PDB; 1H8F; X-ray; A/B=35-386.
 CC PDB; 1I09; X-ray; A/B=1-420.
 CC PDB; 1J1B; X-ray; A/B=1-420.
 CC PDB; 1J1C; X-ray; A/B=1-420.
 CC PDB; 1O9U; X-ray; A=35-384.
 CC PDB; 1PYX; X-ray; A/B=1-420.
 CC PDB; 1Q3D; X-ray; A/B=2-420.
 CC PDB; 1Q3W; X-ray; A/B=2-420.
 CC PDB; 1Q41; X-ray; A/B=2-420.
 CC PDB; 1Q4L; X-ray; A/B=2-420.
 CC PDB; 1Q5K; X-ray; A/B=7-420.
 CC PDB; 1R0E; X-ray; A/B=35-420.
 CC PDB; 1UV5; X-ray; A=35-384.
 CC IntAct; P49841; -; Homo sapiens.
 CC Ensembl; ENSG00000082701; Homo sapiens.
 CC H-InvDB; HIX0003589; -.
 CC HGNC; HGNC:4617; GSK3B.
 CC MIM; 605004; gene.
 CC LinkHub; P49841; -.
 CC GO; GO:0004696; F:glycogen synthase kinase 3 activity; TAS.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0005577; P:glycogen metabolism; TAS.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF00069; Pkinase; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
 CC 3D-structure: Alternative splicing; ATP-binding; Kinase;
 CC Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
 CC Transferase; Wnt signaling pathway.
 CC CHAIN 1 420 Glycogen synthase kinase-3 beta.
 CC FT /FTID=PRO_0000085980.
 CC FT DOMAIN 56 340 Protein kinase.
 CC FT NP_BIND 62 70 ATP (By similarity).
 CC FT ACT_SITE 181 181 Proton acceptor.
 CC FT BINDING 85 85 ATP (By similarity).
 CC FT MOD_RES 9 9 Phosphoserine (by PKB/AKT1).
 CC FT MOD_RES 216 216 Phosphotyrosine.
 CC FT MOD_RES 389 389 Phosphoserine (By similarity).
 CC FT MOD_RES 390 390 Phosphothreonine.
 CC FT VARSPPLIC 303 303 K->KDSGCTGFTSGVR (in isoform 2).
 CC FT /FTID=VSP_004790.
 CC FT S->A: Loss of phosphorylation;
 CC FT insensitive to inhibitory
 CC FT phosphorylation.
 CC FT V->G (in Ref. 4).
 CC
 CC CONFLICT 28 28

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FT  CONFLICT  350  350  L -> H (in Ref. 1).
FT  STRAND    38  48

Query Match      96.7%; Score 2013; DB 1; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 70
Db  1 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 60

QY  71 VINGSGVGVYQAKLDCSGLVAIKVLQDKRPNKRELOIMRKLHDCNIVRLRYFFVSSG 130
Db  61 VINGSGVGVYQAKLDCSGLVAIKVLQDKRPNKRELOIMRKLHDCNIVRLRYFFVSSG 120

QY  131 EKDEVVNLVLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 190
Db  121 EKDEVVNLVLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 180

QY  191 DIKPNLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 250
Db  181 DIKPNLLDPDTAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFGATDYTSIDV 240

QY  251 WSAGCVLAELLGQIPIPGSGVDOLVEIKVLGTPREQI REMPNYTFKPKQIAHP 310
Db  241 WSAGCVLAELLGQIPIPGSGVDOLVEIKVLGTPREQI REMPNYTFKPKQIAHP 300

QY  311 WTKVFRPTPEALACSLRLVYPTARLTPLCAHSHFDELDPNVKHPNGRDTPALF 370
Db  301 WTKVFRPTPEALACSLRLVYPTARLTPLCAHSHFDELDPNVKHPNGRDTPALF 360

QY  371 NFFTQELSSNPPLATILIPPHARI 394
Db  361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 2
GSK3B_MOUSE
ID  GSK3B_MOUSE  STANDARD;  PRT;  420 AA.
AC  Q9WV60;
DT  01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT  01-MAY-2000, sequence version 2.
DE  Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta).
GN  Name=Gsk3b;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Muridae; Muridae; Muridae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [MRNA].
RC  Tissue=Testis;
RA  Salameh W.A., Guo T.B., Chan K.C., Mitchell A.P.;
RT  "Testicular expression and hormonal control of glycogen synthase
RL  kinase 3, a homologue of yeast RIM1."
RL  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC  STRAIN=Czech II, and FVB/N; TISSUE=Mammary gland;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Vallaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

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RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [3]
RP  PHOSPHORYLATION SITE SER-389, AND MASS SPECTROMETRY.
RX  PubMed=15345747; DOI=10.1074/mcp.M400085-MCP200;
RA  Ballif B.A., Villen J., Beausoleil S.A., Schwartz D., Gygi S.P.;
RT  "Phosphoproteomic analysis of the developing mouse brain."
RL  Mol. Cell. Proteomics 3:1093-1101(2004).
RN  [4]
RP  PHOSPHORYLATION SITE TYR-216, AND MASS SPECTROMETRY.
RX  PubMed=15592455; DOI=10.1038/nbt1046;
RA  Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,
RA  Zha X.-M., Foltakiewicz R.D., Comb M.J.;
RT  "Immunofluorescence profiling of tyrosine phosphorylation in cancer
RT  cells."
RL  Nat. Biotechnol. 23:94-101(2005).
CC  -I- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
CC  the hormonal control of several regulatory proteins including
CC  glycogen synthase, MYB and the transcription factor JUN (By
CC  similarity).
CC  -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -I- SUBUNIT: Monomer. Interacts with NIN (By similarity).
CC  -I- PTM: Phosphorylation on Tyr-216 is necessary for the activity (By
CC  similarity).
CC  -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
CC  subfamily.
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CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
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EMBL; AF156099; AAD39258.2; -; mRNA.
EMBL; BC006936; AAH06936.1; -; mRNA.
EMBL; BC00743; AAH0743.1; -; mRNA.
HSSP; P49841; ICGNG.
SMR; Q9WV60; 23-386.
IntAct; Q9WV60; -.
Ensembl; ENSMUSG0000022812; Mus musculus.
MGI; MGI:1861437; Gsk3b.
GO; GO:0005829; C:cytosol; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:008013; F:beta-catenin binding; IPI.
GO; GO:0050321; P:tau-protein kinase activity; IDA.
GO; GO:0006916; P:anti-apoptosis; IMP.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0045444; P:fat cell differentiation; IDA.
GO; GO:0009887; P:organogenesis; IMP.
GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
GO; GO:0006611; P:protein-nucleus export; IDA.
GO; GO:0000320; P:entry into mitotic cell cycle; IDA.
GO; GO:0006350; P:response to stress; IDA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_kinase.
InterPro; IPR002290; Ser_thr_kinase.
InterPro; IPR001245; Tyr_kinase.
Pfam; PF00089; Kinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW  Serine/threonine-protein kinase; Transferase; Wnt signaling pathway.
FT  CHAIN 1 420 /FTid=PRO_0000085981.
FT  DOMAIN 56 340 protein kinase.
FT  NP_BIND 62 70 ATP (By similarity).
FT  ACT_SITE 181 181 Proton acceptor (By similarity).

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FT BINDING      85      85      ATP (By similarity).
FT MOD_RES      9       9       Phosphoserine (by PRB/AKT1) (By
FT                      similarity).
FT MOD_RES     216     216     Phosphotyrosine.
FT MOD_RES     389     389     Phosphoserine.
SQ SEQUENCE    420 AA; 46710 MW; 200C3FD1B38B4883 CRC64;

Query Match      96.7%; Score 2013; DB 1; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSRLDKGSKVTTVVATPGQGPDRPQSVSYDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSRLDKGSKVTTVVATPGQGPDRPQSVSYDTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLDDPDPAVLKLCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 250
Db 181 DIKPQNLDDPDPAVLKLCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQLVEIIKVLGTPTREQIREMNPNTYEFKFPQKAHP 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQLVEIIKVLGTPTREQIREMNPNTYEFKFPQKAHP 300

QY 311 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
Q6FI27 HUMAN PRELIMINARY; PRT; 420 AA.
AC Q6FI27
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 9.
DE GSK3B protein.
GN Name=GSK3B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkoondinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
CC EMBL; CR536510; CAG38748.1; -; mRNA.
DR SMR; Q6FI27; 23-386.
DR Ensembl; ENSG0000082701; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

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DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR022290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE    420 AA; 46744 MW; 4ACC24D00CDBB9C3 CRC64;

Query Match      96.7%; Score 2013; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSRLDKGSKVTTVVATPGQGPDRPQSVSYDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSPAFSGSMKVSRLDKGSKVTTVVATPGQGPDRPQSVSYDTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSSG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLDDPDPAVLKLCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 250
Db 181 DIKPQNLDDPDPAVLKLCDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQLVEIIKVLGTPTREQIREMNPNTYEFKFPQKAHP 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQLVEIIKVLGTPTREQIREMNPNTYEFKFPQKAHP 300

QY 311 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEAIALCSRLLVETPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4
Q5KU03 MOUSE PRELIMINARY; PRT; 420 AA.
ID Q5KU03_MOUSE
AC Q5KU03
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Glycogen synthase kinase 3 beta/tau protein kinase I (NOD-derived
DE CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library,
DE clone:F630213P21 product:glycogen synthase kinase 3 beta, full insert
DE sequence) (NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone:F630015008 product:glycogen synthase
DE kinase 3 beta, full insert sequence).
GN Name=Gsk3b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sano Y., Nakano A., Hirai K., Ohta S., Yanagisawa M., Sato S.,
RA Imahori K.;
RT "Glycogen synthase kinase 3b gene: complete genomic and cDNA
RT structures.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]

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- RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aldins V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gieger T., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core team) and the PANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX MEDLINE=22334683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito K., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y., Hirokawa T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., Konno H., Kiyosawa T., Nishii K., Katsunari T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [9]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD;
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.;

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RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanishi A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB066114; BAD6827.1; -; mRNA.
DR EMBL; AK170965; BAE42146.1; -; mRNA.
DR EMBL; AK154293; BAE32494.1; -; mRNA.
DR SMR; Q5K003; 23-386.
DR Ensembl; ENSMUSG00000022812; Mus musculus.
DR MGI; MGI:1861437; Gsk3b.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:008013; F:beta-catenin binding; IPI.
DR GO; GO:0050221; F:tau-protein kinase activity; IDA.
DR GO; GO:0006916; P:anti-apoptosis; IMP.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0045444; P:fat cell differentiation; IDA.

Query Match 96.7%; Score 2013; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.1e-148;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSPAECKPQQPSAFGSMKVSVDKSGKVTTVVATPGQDPQPSVYTDTK 70
DB 1 MSGRPRTTSPAECKPQQPSAFGSMKVSVDKSGKVTTVVATPGQDPQPSVYTDTK 60

QY 71 VINGSGFVVYQAKLDSGBELVAKKVLQDKRPNRLEQIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFVVYQAKLDSGBELVAKKVLQDKRPNRLEQIMRKLDHCNIVRLRYFFYS 120

QY 131 EKDEVYLNVLVDVPTVYRVARHYSRAKQTLPIVIVKLYQLFSLAYIHSFGICHR 190
DB 121 EKDEVYLNVLVDVPTVYRVARHYSRAKQTLPIVIVKLYQLFSLAYIHSFGICHR 180

QY 191 DIKPNLLDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 181 DIKPNLLDPTAVLKLCDPFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLLGQIPPGSGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKFPQKAHP 310
DB 241 WSAGCVLAELLLGQIPPGSGVDQLVEIIVKVLGTPTRQIREMNPNTYEFKFPQKAHP 300

QY 311 WTKVFRPTPEALALCSRLLEVTPTARLPLACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEALALCSRLLEVTPTARLPLACAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 5
GSK3B RAT
ID GSK3B RAT STANDARD; PRT; 420 AA.
AC P18266;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 61.
DE Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta) (Factor A)
DE (FA).
GN Name=Gsk3b;
```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=90316097; PubMed=2164470;
RA Woodgett J.R.;
RT "Molecular cloning and expression of glycogen synthase kinase-3/factor
RT A.";
RL EMBL J. 9:2431-2438(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=93307488; PubMed=7686508; DOI=10.1016/0014-5793(93)81066-9;
RA Ishiguro K., Shiratsuchi A., Sato S., Omori A., Arioka M.,
RA Kobayashi S., Uchida T., Imahori K.;
RT "Glycogen synthase kinase 3 beta is identical to tau protein kinase I
RT generating several epitopes of paired helical filaments.";
RL FEBS Lett. 325:167-172(1993).
RN [3]
RP PHOSPHORYLATION SITE TYR-216.
RX MEDLINE=93178457; PubMed=8382613;
RA Hughes K., Nikolakaki E., Plyte S.E., Totty N.F., Woodgett J.R.;
RT "Modulation of the glycogen synthase kinase-3 family by tyrosine
RT phosphorylation.";
RL EMBL J. 12:803-808(1993).
CC -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
CC the hormonal control of several regulatory proteins including
CC glycogen synthase, MYB and the transcription factor JUN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBUNIT: Interacts with NIN (By similarity). Monomer.
CC -1- PTM: Phosphorylation of Tyr-216 is necessary for the activity.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
CC subfamily.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X53428; CAA37519.1; -; mRNA.
DR EMBL; X73653; CAA52020.1; -; mRNA.
DR PIR; S14708; TVRTXB.
DR HSP; P49841; 1109.
DR SMR; P18266; 23-386.
DR Ensembl; ENSRNOG00000002833; Rattus norvegicus.
DR RGD; 70982; Gsk3b.
DR GO; GO:0004696; F:glycogen synthase kinase 3 activity; IDA.
DR GO; GO:0005515; F:protein binding; IDA.
DR GO; GO:0030010; P:establishment of cell polarity; IDA.
DR GO; GO:0006917; P:induction of apoptosis; IDA.
DR GO; GO:0045892; P:negative regulation of transcription, DNA-d. .; IDA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR01245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase; Wnt signaling pathway.
FT CHAIN 1 420 Glycogen synthase kinase-3 beta.
FT /FTID=PRO_0000085982.
FT DOMAIN 56 340 Protein kinase.
FT NP_BIND 62 70 ATP (By similarity).
FT ACT_SITE 181 181 Proton acceptor (By similarity).
FT BINDING 85 85 ATP (By similarity).
FT MOD_RES 9 9 Phosphoserine (by PKB/AKT1) (By
FT similarity).
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FT MOD_RES 216 216 Phosphotyrosine.
FT MOD_RES 389 389 Phosphoserine (By similarity).
FT MUTAGEN 216 216 Y->F: Loss of phosphorylation.
FT CONFLICT 240 240 M -> V (in Ref. 2).
SQ SEQUENCE 420 AA; 46742 MW; 2F473FCAB89B4398 CRC64;

Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 7.1e-148;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCKPVQPSAFGSMKVSRRDQSGKVTTVATPGGPDPRPOBVSVDTK 70
Db 1 MSGRPRTTTFAESCKPVQPSAFGSMKVSRRDQSGKVTTVATPGGPDPRPOBVSVDTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPTAVLKLDFGSAKQVLRGEPNVSVICRYRRAPELIFGATDYSIDV 250
Db 181 DIKPNLLDPTAVLKLDFGSAKQVLRGEPNVSVICRYRRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQPIFGDQVQLVEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 310
Db 241 WSAGCVLAELLGQPIFGDQVQLVEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 300

QY 311 WTKVFRPTPPPEAIALCSRLLEVTPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPPPEAIALCSRLLEVTPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 6
Q5XJC2_SPECI PRELIMINARY; PRT; 420 AA.
AC Q5XJC2;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Glycogen synthase kinase 3 beta.
OS Spermophilus citellus (European suslik) (Citellus citellus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Scuridae; Xerinae; Marmotini; Spermophilus.
OX NCBI_TaxID=9997;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stieler J.T., Strijkstra A.M.;
RT "Molecular cloning of Spermophilus citellus glycogen synthase kinase 3 beta.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY392021; AAS59774.1; -; mRNA.
DR SMR; Q5XJC2; 23-386
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46744 MW; 5F5243CA7D9EA549 CRC64;

Query Match 96.4%; Score 2006; DB 2; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.5e-147;
Matches 382; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 MSGRPRTTTFAESCKPVQPSAFGSMKVSRRDQSGKVTTVATPGGPDPRPOBVSVDTK 70
Db 1 MSGRPRTTTFAESCKPVQPSAFGSMKVSRRDQSGKVTTVATPGGPDPRPOBVSVDTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPTAVLKLDFGSAKQVLRGEPNVSVICRYRRAPELIFGATDYSIDV 250
Db 181 DIKPNLLDPTAVLKLDFGSAKQVLRGEPNVSVICRYRRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQPIFGDQVQLVEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 310
Db 241 WSAGCVLAELLGQPIFGDQVQLVEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 300

QY 311 WTKVFRPTPPPEAIALCSRLLEVTPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPPPEAIALCSRLLEVTPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 7
Q9IBD2_BRARE PRELIMINARY; PRT; 421 AA.
AC Q9IBD2;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Glycogen synthase kinase 3 beta.
GN Name=gsk3b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RA Shimizu T., Yamana Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibiki M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RL formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB032265; BAA92442.1; -; mRNA.
DR HSSP; P49841; 1109.


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DR SMR; Q9YH60; ENSDARG0000017803; Danio rerio.
DR ZFIN; ZDB-GENE-990714-4; gsk3b.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46856 MW; 2B251B4C660C00EB CRC64;

Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 6.7e-144;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 11 MSGRPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVATPGGDPDRPQEVSYTDTK 70
Db 1 MSGRPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVATPGGDPDRPQEVSYTDK 60

QY 71 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYS 130
Db 61 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYS 120

QY 131 EKDEYVLNLVDYVPETVVRVARYSRAKQTLPIVYVKLYMQLPRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVVRVARYSRAKQTLPIVYVKLYMQLPRSLAYIHSFGICHR 180

QY 191 DIKPQNLDDPDTAVLKCLDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYSIDV 250
Db 181 DIKPQNLDDPDTAVLKCLDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 300

QY 311 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFTTQELSSNPPLATILIPPHAR 393
Db 361 NFTTQELSSNPPLATILIPPHAR 383

RESULT 8
QYH60_BRARE PRELIMINARY; PRT; 421 AA.
ID Q9YH60;
AC Q9YH60;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Glycogen synthase Kinase 3.
GN Name=gsk3b; Synonyms=GSK3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;

RT "Differential expression of glycogen synthase kinase 3 genes during
RL zebrafish embryogenesis.";
RL Mech. Dev. 91:387-391(2000).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AJ223502; CAA11420.1; -; mRNA.
DR SMR; P49841; 1109.
DR HSP; Q9YH60; 23-386.
DR Ensembl; ENSDARG0000017803; Danio rerio.
DR ZFIN; ZDB-GENE-990714-4; gsk3b.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46872 MW; 2B251B4C7B6C00EB CRC64;

Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 6.7e-144;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 11 MSGRPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVATPGGDPDRPQEVSYTDTK 70
Db 1 MSGRPRTTFAESCKPVQPSAFGSMKVS RDKGSKVTTVATPGGDPDRPQEVSYTDK 60

QY 71 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYS 130
Db 61 VINGSGFVVYQAKLDSGELVAIKVLDQKRFKRELQIMRKLDHCNIVRLRYFFYS 120

QY 131 EKDEYVLNLVDYVPETVVRVARYSRAKQTLPIVYVKLYMQLPRSLAYIHSFGICHR 190
Db 121 EKDEYVLNLVDYVPETVVRVARYSRAKQTLPIVYVKLYMQLPRSLAYIHSFGICHR 180

QY 191 DIKPQNLDDPDTAVLKCLDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYSIDV 250
Db 181 DIKPQNLDDPDTAVLKCLDFGSAKQLVRGEPNVSYCSRYRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTRQIREMNPNTYEFKPPQKAHP 300

QY 311 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEAIALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFTTQELSSNPPLATILIPPHAR 393
Db 361 NFTTQELSSNPPLATILIPPHAR 383

RESULT 9
Q91757_XENLA PRELIMINARY; PRT; 420 AA.
ID Q91757;
AC Q91757;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Intracellular kinase (Xgsk-3 protein).

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GN Name=Xgsk-3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95237008; PubMed=7720580;
RA Pierce S.B., Krimelman D.;
RT "Regulation of Spemann organizer formation by the intracellular kinase
RT Xgsk-3".
RL Development 121:755-765 (1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Embryo;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Wagner J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative".
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC ENBL; L38492; AAC42224.1; -; mRNA.
CC ENBL; BC108581; AA108582.1; -; mRNA.
CC PIR; I51425; I51425.
CC HSSP; P49841; I109.
CC SMR; Q91757; 23-386.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0000166; F:nucleotide binding; IEA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.
CC GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser Thr_pkin AS.
CC InterPro; IPR002290; Ser Thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00069; Pkinase; I.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS0108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46903 MW; C02280B8A35785D CRC64;
[1]
Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 1e-141;
Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
Qy 11 MSGRPRTTSFAESCKPVQOPSAFGSMKVSVDKDGSKVTIVVATPGQGPDRPQSVYTDTK 70
Db 1 MSGRPRTTSFAESCKPVQOPSAFGSMKVSVDKDGSKVTIVVATPGQGPDRPQSVYTDTK 60
Qy 71 VINGSGFVVYQAKLDCGSELVAIKVLDQRFKNRELIMRKLHCHNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCGSELVAIKVLDQRFKNRELIMRKLHCHNIVRLRYFFYSYG 120
Qy 131 EKDEVYLVLDVYPETVYRVARHYHSAKQTLPIVYVKLYMYQLFRSLAYIHSGFCHR 190
Db 121 EKDEVYLVLDVYPETVYRVARHYHSAKQALPIIYVKLYMYQLFRSLAYIHSGFCHR 180
Qy 191 DIKPQNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDVTSSIDV 250
Db 181 DIKPQNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSYRYRAPELIFGATDVTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFPDGSVDQLVEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAHP 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQLVEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAHP 300
Qy 311 WTKVFRPTPEAIACSRLLVETPTARLPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEAIACSRLLVETPTARLPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTQELSSNPPLATILIPPHAR 393
Db 361 NFTTQELSSNPPLATILIPPHAR 383
RESULT 10
Q91627 XENLA
ID Q91627 XENLA PRELIMINARY; PRT; 420 AA.
AC Q91627;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Glycogen synthase kinase 3 beta.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95396823; PubMed=7667318;
RA Dominguez I., Itoh K., Sokol S.Y.;
RT "Role of glycogen synthase kinase 3 beta as a negative regulator of
RT dorsoventral axis formation in Xenopus embryos".
RL Proc. Natl. Acad. Sci. U.S.A. 92:8498-8502 (1995).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC ENBL; U31862; AAA84444.1; -; mRNA.
CC PIR; I51692; I51692.
CC HSSP; P49841; I109.
CC SMR; Q91627; 23-386.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0000166; F:nucleotide binding; IEA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
CC GO; GO:0016740; F:transferase activity; IEA.

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DR GO: 00006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008270; Ser_thr_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46900 MW; 4FECEA381835BF07 CRC64;

Query Match 92.4%; Score 1923; DB 2; Length 420;
Best Local Similarity 95.0%; Pred. No. 4.2e-141;
Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 11 MSGRPRTTSPAESCKPVQPSAFSGSMKVSRRDKGSKVTTTVAATPGQGPDRPQEVSYDTDK 70
Db 1 MSGRPRTTSPAESCKPVQPSAFSGSMKVSRRDKGSKVTTTVAATPGQGPDRPQEVSYDTDK 60

QY 71 VIGNGSFGVYVYQAKLDCSGELVAIKVQLDQKRFKNRELQIMRKLDHCNIVRLRYFFVSSG 130
Db 61 VIGNGSFGVYVYQAKLDCSGELVAIKVQLDQKRFKNRELQIMRKLDHCNIVRLRYFFVSSG 120

QY 131 EKDEVLNLVLDVYPETVYVYRVARHYSRAKQTLPIVYVYKLYMQLFRSLAYTHSFGICHR 190
Db 121 EKDEVLNLVLDVYPETVYVYRVARHYSRAKQALPIVYVYKLYMQLFRSLAYTHSFGICHR 180

QY 191 DIKPNLLDPDTAVLKLDCFGSAKQLVRGEPNVSYICSYRYAPELIFGATDYSIDV 250
Db 181 DIKPNLLDPDTAVLKLDCFGSAKQLVRGEPNVSYICSYRYAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQTPPGDSGVDDVLEIKVLGTPTRBQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQTPPGDSGVDDVLEIKVLGTPTRBQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTPEALCSRLLEVTPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEALCSRLLEVTPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFTQELSSNPPLATILIPHAR 393
Db 361 NFTQELSSNPPLSSILIPAHAR 383

RESULT 11
Q4SOHO_TETNG PRELIMINARY; PRT; 496 AA.
AC Q4SOHO;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Chromosome 2 SCF14781, whole genome shotgun sequence.
GN ORFNames=GSTENG00026022001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

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RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN [2]
RG NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -! SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -! SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: CAAB01014781; CAG05862.1; -; Genomic_DNA.
DR SNR; Q4SOHO; 32-133.
DR GO: 00005524; F:ATP binding; IEA.
DR GO: 0000166; F:nucleotide binding; IEA.
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: 0016740; F:transferase activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 496 AA; 55961 MW; 4C86362BD3301390 CRC64;

Query Match 86.2%; Score 1793.5; DB 2; Length 496;
Best Local Similarity 73.8%; Pred. No. 6.3e-131;
Matches 354; Conservative 8; Mismatches 3; Indels 115; Gaps 3;

QY 11 MSGRPRTTSPAESCKPVQPSAFSGSMKVSRR-----DKGSKVTTTVAATPGQGPDRP 61
Db 1 MSGRPRTTSPAESCKPVQPSAFSGSMKVSQTLNPGWRGDKGSKVTTTVAATPGQGPDRP 60

QY 62 QEVSYTDTKVIKNGSFGVYVYQAKLDCSGELVAIKVQLDQKRFKNRELQIMRKLDHCNIVR 121
Db 61 QEVSYTDTKVIKNGSFGVYVYQAKLDCSGELVAIKVQLDQKRFKNRELQIMRKLDHCNIVR 120

QY 122 LRYFFYSYSGEK----- 132
Db 121 LRYFFYSYSGDKPDRANRPPSSVNVSVTVGELSQWLRCPCSQLTRARVAAGSGSEPIR 180

QY 133 -----KDBVYNLNLVDYV 145
Db 181 PSNGQPKWLCRCGRKRSLTFLRESANKRVDIPQVPRSRGHSVRSKDBVYNLNLVDYV 240

QY 146 PETVYVYRVARHYSRAKQTLPIVYVYKLYMQLFRSLAYTHSFGICHRDKPQNLLDPDTAV 205
Db 241 PETVYVYRVARHYSRAKQTLPIVYVYKLYMQLFRSLAYTHSFGICHRDKPQNLLDPDTAV 300

QY 206 LKLCDFGSAKQLVRGEPNVSYICSYRYAPELIFGATDYSIDVWSAGCVLAELLGQIP 265

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Db 301 LKLCDFGSAKQVRGPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLIGQP 360
 QY 266 IFPGDSGVQDLVEIK-----VLGTPTRQIREMNPNTYEFKFPQIKAHPTWKVF 315
 Db 361 IFPGDSGVQDLVEIKRQNAARSPQVLGTPTRQIREMNPNTYEFKFPQIKAHPTWKVF 420
 QY 316 RPTPEATALCSRLLEYTPARTLPLEACAHGFFDELDPNVKHPNGRDTPALFNFTTQ 375
 Db 421 RPTPEATALCSRLLEYTPARTLPLEACAHGFFDELDPNVKHPNGRDTPALFNFTTQ 480

RESULT 12
 Q9YH61_BRARE
 ID Q9YH61_BRARE PRELIMINARY; PRT; 440 AA.
 AC Q9YH61;
 DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 38.
 DE Glycogen synthase kinase 3 alpha.
 GN Name-gsk3a; Synonyms=GSK3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
 RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;
 RT "Differential expression of glycogen synthase kinase 3 genes during
 zebrafish embryogenesis.";
 RL Mech. Dev. 91:387-391 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RG NIH NIG Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC
 CC EMBL; AJ223501; CAA11419.1; -; mRNA.
 CC EMBL; BC056332; AAH56332.1; -; mRNA.

DR HSP; P49841; 1Q3W.
 DR SMR; Q9YH61; 52-412.
 DR Ensembl; ENSDARG00000015681; Danio rerio.
 DR ZFIN; ZDB-GENE-990714-3; Gsk3a.
 DR GO; GO:000524; F:ATP binding; IEA.
 DR GO; GO:000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; prot kinase.
 DR InterPro; IPR008271; Ser_Thr_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 440 AA; 48065 MW; 66A8E8D070ACA093 CRC64;
 Query Match 81.9%; Score 1704.5; DB 2; Length 440;
 Best Local Similarity 79.1%; Pred. No. 4.7e-124;
 Matches 326; Conservative 26; Mismatches 25; Indels 35; Gaps 3;
 QY 12 SGRPTTSSAESCKPVQQP-----SAFGSMKVSRD 41
 Db 4 SGRPTSSFAE---PGVFGAAAAAGSAGSSSGKTGGAQAGSSSGFGNKLGR- 59
 QY 42 KDGSKVTVVATPGQGPDRPQEVSYTDTKVIGNSGFVVYQAKLSDGELVAIKVLQDK 101
 Db 60 -DSGKVTTVVATPGQGPDRPQEVSYTDTKVIGNSGFVVYQAKLSDGELVAIKVLQDK 118
 QY 102 RFKNRELQIMRKLDHCNIVRLRYFFYSKGEKDEVLNVLVDVVPVTVVVAHYHRAKQ 161
 Db 119 RFKNRELQIMRKLDHCNIVRLRYFFYSKGEKDEVLNVLVDVVPVTVVVAHYHRAKSKT 178
 QY 162 TLPVIVVLYVMYQFSLAYIHSFGICHRDIPQNLDDPDTAVLKLDFGSAKQLVRGE 221
 Db 179 TPIIIVKVMYQLFRSLAYIHSQGVCHRDIPQNLDDPDTAVLKLDFGSAKQLVRGE 238
 QY 222 PNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLIGQIFPGDSGVQDLVEIK 281
 Db 239 PNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLIGQIFPGDSGVQDLVEIK 298
 QY 282 VLGTPTREQIREMNPNTYEFKFPQIKAHPTWKVFRPTPEALCSRLLEYTPARTLTP 341
 Db 299 VLGTPTREQIREMNPNTYEFKFPQIKAHPTWKVFRPTPEALCSRLLEYTPARTLTP 358
 QY 342 LEACAHGFFDELDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR 393
 Db 359 LEACAHGFFDELDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHAR 410

RESULT 13
 Q9IBD3_BRARE
 ID Q9IBD3_BRARE PRELIMINARY; PRT; 435 AA.
 AC Q9IBD3;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 07-FEB-2006, entry version 26.
 DE Glycogen synthase kinase 3 alpha.
 GN Name-gsk3a;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RA Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Iabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; A8032264; BAA92441.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMR; Q9NLA3; 52-412.
DR Ensembl; ENSDARG00000015681; Danio rerio.
DR ZFIN; ZDB-GENE-990714-3; gsk3a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.
DR PROSITE; PS0011; PROTEIN KINASE ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 435 AA; 47791 MW; ED7793A03D8C706 CRC64;

Query Match 80.2%; Score 1669.5; DB 2; Length 435;
Best Local Similarity 78.2%; Pred. No. 2.4e-121;
Matches 322; Conservative 26; Mismatches 29; Indels 35; Gaps 3;

QY 12 SGRPRTTTSAESCKPVQPP-----SAGSMKVSRD 41
DB 4 SGRPRTTSPAE---PPGVPGAAAAAGSAVAGSSSGKTGGAQAGSGSSGFGNLKGR- 59

QY 42 KDSKUTTVVATPGQDPDRPQVSYTDTKVIKNGSGFVGYVQAKLDSGELVAIKVLQDK 101
DB 60 -DSGKUTTVVATPGQDPDRPQVSYTDTKVIKNGSGFVGYVQAKLDSGELVAIKVLQDK 118

QY 102 RFKNRELQIMRKLDHCNIVRLRYFFYSSEKDEVLNLDVYVPTVYVARHYSRAKQ 161
DB 119 RFKNRELQIMRKLDHCNIVRLRYFFYSSEKDEVLNLDVYVPTVYVARHYSRAKQ 178

QY 162 TLPVIYVKLYMYQLFRSLAYIHSGICHRIKDPQNLLDPDPTAVLKLDFGSAKQLVRGE 221
DB 179 TILYIVKLYMYQLFRSLAYIHSGICHRIKDPQNLLDPDPTAVLKLDFGSAKQLVRGE 238

QY 222 PNVSYICSRYPAPLIFGATDYSIDVWSAGCVLAELLGQPIPPGSGVDOLVEIK 281
DB 239 PNVSYICSRYPAPLIFGATDYSIDVWSAGCVLAELLGQPIPPGSGVDOLVEIK 298

QY 282 VLGTPTREQIREMNPNTYEFKPKQIAHPMTKVFPRTPPEALCSRLLEYTPPTARLTP 341
DB 299 VLGPXTREQIREMNPNTYEFKPKQIAHPMTKVFPRTPPEALCSRLLEYTPPTARLTP 358

QY 342 LEACAHFFDELDPNVKHPNGRDTPALFNPFTTQELSSNPPLATILIPPHAR 393
DB 359 LEACAHFFDELDPNVKHPNGRDTPALFNPFTTQELSSNPPLATILIPPHAR 410

RESULT 14
Q9NLA3 CIOIN
ID Q9NLA3 CIOIN PRELIMINARY; PRT; 407 AA.
AC Q9NLA3;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.

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DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 32.
DE Glycogen synthase kinase alpha/beta.
GN Name=CiGSK; Synonyms=Ci-GSK alpha/beta;
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Imai K., Takada N., Satoh N., Satou Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pubmed=16252120; DOI=10.1007/s00427-005-0016-9;
RX Satou Y., Satoh N.;
RT "Cataloging transcription factor and major signaling molecule genes
RT for functional genomic studies in Ciona intestinalis.";
RL Dev. Genes Evol. 215:580-596(2005).
CC -----
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CC -----
DR EMBL; AB031544; BAA92186.1; -; mRNA.
DR EMBL; AB211133; BAE06824.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMR; Q9NLA3; 9-368.
DR Ensembl; ENSCING000000001821; Ciona intestinalis.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 407 AA; 45566 MW; E71594A9B6B59F10 CRC64;

Query Match 80.1%; Score 1666.5; DB 2; Length 407;
Best Local Similarity 83.0%; Pred. No. 3.8e-121;
Matches 318; Conservative 24; Mismatches 26; Indels 15; Gaps 2;

QY 11 MSGRPRTTTSAESCKPVQPPSAGSMKVSRRDKGKVTWATPGQDPDRPQVSYTDTK 70
DB 1 MGAAPKT-----LGNMKSRLDE-SKITTVVATHGHPDRPQEVATDTK 45

QY 71 VIGNGSGFVGYVQAKLDSGELVAIKVLQDKPFKNRELQIMRKLDHCNIVRLRYFPYSSG 130
DB 46 VIGNGSGFVGYVQARLIESNEWAIKKVLQDKPFKNRELQIMRKLDHCNIVRLRYFPYSSG 105

QY 131 EKDEVLNLDVYVPTVYVARHYSRAKQITPLVYVKLYMYQLFRSLAYIHSGICHRI 190
DB 106 DKDEVLNLDVYVPTVYVARHYSRAKQITPLVYVKLYMYQLFRSLAYIHSGICHRI 165

QY 191 DIKPNLLDPDPTAVLKLDFGSAKQLVRGEPNVSYICSRYPAPLIFGATDYSIDV 250
DB 166 DIKPNLLDPDPTAVLKLDFGSAKQLVRGEPNVSYICSRYPAPLIFGATDYSIDV 225

QY 251 WSAGCVLAELLGQPIPPGSGVDOLVEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 310
DB 226 WSAGCVLAELLGQPIPPGSGVDOLVEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 285

QY 311 WTKVFRPRTPEALCSRLLEYTPPTARLTPLEACAHFFDELDPNVKHPNGRDTPALF 370
DB 286 WSKVFRPRTPEALCSRLLEYTPPNRISPLESCAHFFDELRLPNTKLPNGRSPLPLF 345

QY 371 NFFTQELSSNPPLATILIPPHAR 393

```

Qy 252 SAGCVLAELLLGQPIPPGDSGVDQVLEIIKVLGTPTEQIREMNPNTYEFKFOIKAHPW 311
 Db 242 SAGCVLAELLLGQPIPPGDSGVDQVLEIIKVLGTPSRDQIKEMNPNTYEFKFOIKAHPW 301
 Qy 312 TKVPRRTPEATACSRLLLEYTPARLTPLEACAHSSFFDELDRDPNVKHNGRDTPALEN 371
 Db 302 SKVFRTRTPADALQCSRLLLEYTPKSRIKPLEACAHQFSELDRDPGKLPNGRELPLFN 361
 Qy 372 FTTQELSSNPPLATILIPPH 391
 Db 362 FTAGELASKPSLRTALIPPH 381

Search completed: September 15, 2006, 17:12:10
 Job time : 306 secs

Db 346 NPTDKELSIKSPNLNLIPLHAR 368
 RESULT 15
 Q6IUG5_LYTVA
 ID Q6IUG5_LYTVA PRELIMINARY; PRT; 414 AA.
 AC Q6IUG5;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE Glycogen synthase kinase-3.
 GN Names-GSK-3;
 OS Lytechinus variegatus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7654;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA PubMed=15151983; DOI=10.1242/dev.01152;
 RA Weitzel H.E., Illies M.R., Byrum C.A., Xu R., Wikramanayake A.H.,
 RA Ettensohn C.A.;
 RT "Differential stability of {beta}-catenin along the animal-vegetal
 axis of the sea urchin embryo mediated by dishevelled.";
 RL Development 131:2947-2956(2004).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 DR EMBL; AY624076; AAT42372.1; -; mRNA.
 DR HSSP; P24941; 1AQ1.
 DR SMR; Q6IUG5; 23-381.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 414 AA; 46202 MW; 276988692DF90815 CRC64;
 Query Match 78.4%; Score 1632; DB 2; Length 414;
 Best Local Similarity 80.5%; Pred. No. 1.9e-118;
 Matches 306; Conservative 35; Mismatches 37; Indels 2; Gaps 1;
 Qy 12 SGRPRTTSPAESCKPVQCPQAFGSMKVSVDKSGKVTTVVATPCQGPDPQEVSYDTKV 71
 Db 4 SGRPRTTSPADNR--GSTSSYGLKVRDKDSKITSVTATGPPDPRTKELSYDTRV 61
 Qy 72 IGNGSFGVWYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSSE 131
 Db 62 IGNGSFGVWYQARWVDNDLVAIKKVLQDKRFKNRELQIMRDLDDHNIIVKLYFFYSSE 121
 Qy 132 KDEVYLNVLVDYVPETVYVARHYSRAKOTLPVYVYKLYMYQLFRSLAYIHSGICHRD 191
 Db 122 KDEVFLNLVLEYVPTVYVARHYSRAKOTISLIYVYKLYMYQLFRSLAYIHSGICHRD 181
 Qy 192 IKPQNLLLDPDTAVLKLDFGSAKQVLRGEPNYSYICSRYYRAPELIFGATDYTSIDVW 251
 Db 182 IKPQNLNLLNPETAVALKLDFGSAKQVLRGEPNYSYICSRYYRAPELIFGATDYTCIDVW 241

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:03:15 ; Search time 195 Seconds
(without alignments)
923.812 Million cell updates/sec

Title: US-10-733-816-2
Perfect score: 2081
Sequence: 1 MEWMEGGMSGRPRRTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_8.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*
 - 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2081	100.0	394	5	Abb07578 Human tru
2	2024	97.3	420	4	Aae05998 Human gly
3	2024	97.3	420	5	Abb07577 Human gly
4	2024	97.3	420	7	AbR44294 Human gly
5	2024	97.3	420	7	Adk11467 Human gly
6	2024	97.3	420	8	Adh09637 Human hos
7	2024	97.3	420	8	AdR40191 Human gly
8	2024	97.3	420	8	AdS92965 Glycogen
9	2024	97.3	420	8	AdT92555 Human gly
10	2013	96.7	414	8	AdR06333 p38-alpha
11	2013	96.7	420	2	AR61327 Tau-prote
12	2013	96.7	420	5	Abb77875 Amino aci
13	2013	96.7	420	6	Abp70714 Human gly
14	2013	96.7	420	7	AbR44293 Human gly
15	2013	96.7	420	7	AdD68742 Rat tau p
16	2013	96.7	420	7	AdE64053 Human pro
17	2013	96.7	420	8	Adh09634 Human hos
18	2013	96.7	420	8	AdR06320 Gsk-3 bet
19	2013	96.7	420	8	AdR06317 Gsk-3 bet
20	2013	96.7	420	9	AdY64106 Human gly
21	2013	96.7	420	9	Aea39562 Human gly
22	2013	96.7	420	9	Aea39564 Mouse gly
23	2013	96.7	420	9	Aeb28124 Human gly

24	2013	96.7	420	9	Aec81932 Human gly
25	2013	96.7	420	9	Aee06398 Glycogen
26	2013	96.7	428	7	ADC50594 Human tau
27	2010	96.6	420	2	AAR61326 Tau-prote
28	2010	96.6	420	6	ABR82106 Human gly
29	2010	96.6	420	7	ABR44289 Human gly
30	2010	96.6	420	7	ADE64051 Rat Prote
31	2010	96.6	420	8	ADI28893 Mouse gly
32	1996.5	95.9	433	7	ABR44295 Human gly
33	1996.5	95.9	433	7	ABR44298 Human gly
34	1996.5	95.9	433	7	ADJ69554 Human hea
35	1996.5	95.9	433	8	ADH09633 Human hos
36	1996.5	95.9	433	8	ADO49107 Human ded
37	1996.5	95.9	433	8	ADU20919 Human gly
38	1996.5	95.9	433	8	ADU06409 Novel bro
39	1996.5	95.9	433	9	ABE25735 Human and
40	1996.5	95.9	433	9	AEC34201 Human GSK
41	1996.5	95.9	433	9	AEE06396 Glycogen
42	1996.5	95.9	439	8	ADR66057 Human pro
43	1994.5	95.8	439	8	ADR66399 Human pro
44	1978	95.1	385	9	ADY85481 Catalytic
45	1919	92.2	387	9	AEE06402 Glycogen

ALIGNMENTS

RESULT 1
ABB07578
ID ABB07578 standard; protein; 394 AA.
XX
AC ABB07578;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human truncated GSK3beta polypeptide 557.
XX
KW GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; nootropic; human;
KW Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Peptide i..10
FT /note= "Glu-tag and Gly linker"
FT Peptide 11..394
FT /note= "truncated GSK3beta"
XX
PN W0200210357-A2.
XX
PD 07-FEB-2002.
XX
PF 25-JUL-2001; 2001WO-US023539.
XX
PR 27-JUL-2000; 2000US-0221242P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY;
PI Coit DG, Nguyen SH, Medina-Selby A;
XX
DR WPI; 2002-188732/24.
XX
XX
PT New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids
PT encoding them, useful for treating diseases mediated by GSK3 activity,
PT including Alzheimer's disease, type 2 diabetes and inflammation.
XX
PS Claim 8; Fig 2A-B; 36pp; English.
XX
CC The invention provides glycogen synthase kinase 3 (GSK3) polypeptides
CC capable of crystallisation, including GSK3alpha and GSK3beta
CC polypeptides. The GSK polypeptides can be used to identify and optimise
CC GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as

CC pharmaceutical agents, for treating diseases mediated by GSK3 activity,
 CC including Alzheimer's disease, type 2 diabetes and inflammation. The
 CC present sequence represents the amino acid sequence of a truncated
 CC GSK3beta polypeptide 557
 XX
 SQ Sequence 394 AA;
 Query Match 100.0%; Score 2081; DB 5; Length 394;
 Best Local Similarity 100.0%; Pred. No. 2,9e-216;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEYMPMGSGGSGRPTTSFAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDR 60
 DB 1 MEYMPMGSGGSGRPTTSFAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDR 60
 QY 61 PQEVSYTDTKVIGNGSGVGVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIV 120
 DB 61 PQEVSYTDTKVIGNGSGVGVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIV 120
 QY 121 RLRYFFYSGGEKKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLA 180
 DB 121 RLRYFFYSGGEKKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLA 180
 QY 181 YIHSFGICHRDIKQNLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFG 240
 DB 181 YIHSFGICHRDIKQNLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFG 240
 QY 241 ATDYTSIDVMSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTREQIREMNPYTE 300
 DB 241 ATDYTSIDVMSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTREQIREMNPYTE 300
 QY 301 FKFPQIKAHPTKVFRTPTPEALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKH 360
 DB 301 FKFPQIKAHPTKVFRTPTPEALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKH 360
 QY 361 PNGRDTALFNFTTQELSSNPPLATILIPPHARI 394
 DB 361 PNGRDTALFNFTTQELSSNPPLATILIPPHARI 394
 RESULT 2
 AA05998
 ID AA05998 standard; protein; 420 AA.
 XX
 AC AA05998;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Human glycogen synthase kinase 3-beta #1.
 XX
 KW Antisense; glycogen synthase kinase 3-beta; GSK3B; diabetes; infection;
 KW insulin regulation disorder; neurological disorder; Alzheimer's disease;
 KW bipolar illness; inflammation; tumour; tau protein kinase I; TPK-1;
 KW human.
 XX
 OS Homo sapiens.
 XX
 PN WO200152862-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001085.
 XX
 PR 19-JAN-2000; 2000US-00489765.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Butler MM, McKay R, Monia BP, Wyatt JR;
 XX
 DR WPI; 2001-457510/49.
 DR N-PSDB; AAD11491.
 XX
 PT Novel antisense compounds, particularly antisense oligonucleotides for

PT inhibiting expression of glycogen synthase kinase 3 beta in cells and for
 PT diagnosing, treating neurological and insulin regulation disorders.
 XX
 PS Example 13; Page 88-90; 106pp; English.
 XX

CC The invention relates to antisense compounds targetted to nucleic acid
 CC encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau
 CC protein kinase I (TPK-I)). The antisense compound is useful for
 CC inhibiting the expression of glycogen synthase kinase 3-beta enzyme in
 CC cells or tissues and for treating diseases or conditions associated with
 CC the enzyme such as insulin regulation disorder, in particular diabetes
 CC and neurological disorder, e.g. Alzheimer's disease and bipolar illness.
 CC The antisense compound is also useful for diagnosing diseases associated
 CC with the expression of glycogen synthase kinase 3-beta and for
 CC prophylaxis e.g. to prevent or delay infection, inflammation or tumour
 CC formation and as a research reagent. The present sequence is human
 CC glycogen synthase kinase 3-beta
 XX

SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 4; Length 420;
 Best Local Similarity 100.0%; Pred. No. 5e-210;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDRPQBSVYTDK 70
 DB 1 MSGRPRTTSFAESCKPVQPSAFGSMKVRDQSGKVTTVVATPGQGPDRPQBSVYTDK 70
 QY 71 VIGNGSGVGVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIVLRYFFYS 130
 DB 61 VIGNGSGVGVVYQAKLDCSGELVAIKKVLQDKRPNRELQIMRKLHCNIVLRYFFYS 120
 QY 131 EKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 190
 DB 121 EKDEVYLNLDVVPETVYRVARHYSRAKQTLPIVYVKLYMQLFRSLAYIHSFGICHR 180
 QY 191 DIKPQNLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
 DB 181 DIKPQNLDDPTAVLKCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
 QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTREQIREMNPYTEFKFPQIKAH 310
 DB 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIKVLGTPTREQIREMNPYTEFKFPQIKAH 300
 QY 311 WTKVFRPTPEALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPCNDRTPALF 370
 DB 301 WTKVFRPTPEALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPCNDRTPALF 360
 QY 371 NFFTQELSSNPPLATILIPPHARI 394
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3

ABB07577

ID ABB07577 standard; protein; 420 AA.

XX

AC ABB07577;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human glycogen synthase kinase 3beta (GSK3beta) polypeptide.

XX

KW GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; neotropic; human;
 KW Alzheimer's disease; antinflammatory; antidiabetic; gene therapy.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Modified-site 216

FT Peptide /note= "phosphorylated"

FT 250..419

FT /note= "specifically claimed fragment"

FT Peptide 278..419
FT /note= "specifically claimed fragment"
FT Peptide 285..384
FT /note= "specifically claimed fragment"
FT Peptide 351..384
FT /note= "specifically claimed fragment"
XX
PN WO200210357-A2.
XX
XX
PD 07-FEB-2002.
XX
XX 25-JUL-2001; 2001WO-US023539.
XX
XX 27-JUL-2000; 2000US-0221242P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY;
PI Coit DG, Nguyen SH, Medina-Selby A;
XX
XX WPI; 2002-188732/24.
XX
XX New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids
PT encoding them, useful for treating diseases mediated by GSK3 activity,
PT including Alzheimer's disease, type 2 diabetes and inflammation.
XX
XX Claim 6; Fig 1A-B; 36pp; English.
XX
XX The invention provides glycogen synthase kinase 3 (GSK3) polypeptides
CC capable of crystallisation, including GSK3alpha and GSK3beta
CC polypeptides. The GSK polypeptides can be used to identify and optimise
CC GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as
CC pharmaceutical agents, for treating diseases mediated by GSK3 activity,
CC including Alzheimer's disease, type 2 diabetes and inflammation. The
CC present sequence represents the amino acid sequence of human GSK3beta
CC polypeptide
XX
XX
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 5e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 MSGRPRTTSAESCCKPVQPSAFGSMKVS RDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSAESCCKPVQPSAFGSMKVS RDGSKVTTVVATPGQGPDRPQEVSYTDTK 60
Qy 71 VINGSGVGVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKL DHCNIVRLRYFFYS 130
Db 61 VINGSGVGVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKL DHCNIVRLRYFFYS 120
Qy 131 EKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 180
Qy 191 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFGSGVDQVLEIIVKLGTPPREQIREMNPNTYEFKFPQIKAHP 310
Db 241 WSAGCVLAELLGQPIFGSGVDQVLEIIVKLGTPPREQIREMNPNTYEFKFPQIKAHP 300
Qy 311 WTKVFRPTTPEALCSRLLEYTPPTARLTPLEACAHSFDFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCSRLLEYTPPTARLTPLEACAHSFDFDELDPNVKHPNGRDTPALF 360
Qy 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 4

ABR44294
ID ABR44294 standard; protein; 420 AA.
XX
AC ABR44294;
XX
DT 18-AUG-2003 (first entry)
XX
DE Human glycogen synthase kinase-3 (GSK3)beta polypeptide.
XX
XX GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
XX KW vulnary; antiarteriosclerotic; GSK3beta; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003038037-A2.
XX
XX 08-MAY-2003.
XX
XX 23-OCT-2002; 2002WO-US033909.
XX
XX 29-OCT-2001; 2001US-0350160P.
XX PR 13-NOV-2001; 2001US-0337905P.
XX
XX (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
XX Walsh K;
XX
XX WPI; 2003-482140/45.
XX
XX Modulating angiogenesis, useful for treating hyperlipidemia, comprises
PT administering an angiogenesis inhibitor/promoter, such as an
PT active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3
PT activator/inhibitor.
XX
XX Disclosure; Page 100-101; 115pp; English.
XX
XX The invention relates to inhibiting/enhancing angiogenesis. The method
CC involves administering to a subject needing the treatment, an
CC angiogenesis inhibitor/promoter, such as an active/inactive glycogen
CC synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,
CC where the angiogenesis modulator is administered to inhibit/enhance
CC angiogenesis in a subject. The methods are useful for treating a
CC condition associated with increased apoptotic cell death of vascular
CC endothelial cells, where the condition is characterized by lesion of
CC blood vessel wall, such as hyperlipidemia, also in the treatment of
CC myocardial infarction and in the promotion of wound healing. The present
CC sequence represents a human GSK3beta polypeptide (GenBank Accession No.
CC S53324)
XX
XX
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 7; Length 420;
Best Local Similarity 100.0%; Pred. No. 5e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 MSGRPRTTSAESCCKPVQPSAFGSMKVS RDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSAESCCKPVQPSAFGSMKVS RDGSKVTTVVATPGQGPDRPQEVSYTDTK 60
Qy 71 VINGSGVGVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKL DHCNIVRLRYFFYS 130
Db 61 VINGSGVGVYQAKLDCSGELVAIKVLODKRFKNRELOIMRKL DHCNIVRLRYFFYS 120
Qy 131 EKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVLNLVDVVPETVYRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSFGICHR 180
Qy 191 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 250
Db 181 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDVTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFGSGVDQVLEIIVKLGTPPREQIREMNPNTYEFKFPQIKAHP 310

Db 241 WSAGCVLAELLGQIPFGDGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 300
 Qy 311 WTKVFRPTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
 Db 301 WTKVFRPTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 5
 ADK11467
 ID ADK11467 standard; protein; 420 AA.
 AC ADK11467;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human glycogen synthase kinase 3 beta protein.
 XX
 KW cytostatic; cardiovascular; immunosuppressive; nephrotropic;
 KW antirheumatic; antiarthritic; dermatological; antipsoriatic;
 KW antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;
 KW cardiovascular disorder; autoimmune disease; glomerulonephritis;
 KW rheumatoid arthritis; dermatological disorder; psoriasis;
 KW inflammatory disorder; malaria; emphysema; alopecia.
 XX
 OS Homo sapiens.
 XX
 PN W02003040301-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 23-OCT-2002; 2002WO-GB004780.
 XX
 PR 05-NOV-2001; 2001GB-00026506.
 PR 27-NOV-2001; 2001GB-00028384.
 PR 11-FEB-2002; 2002GB-00003185.
 XX
 PA (CYCL-) CYCLACEL LTD.
 XX
 PI Deak P, Frenz L, Glover D, Midgley C;
 XX
 DR WPI; 2003-441540/41.
 DR N-PSDB; ADK11466.
 XX
 PT New Drosophila polypeptides and polynucleotides, useful for diagnosing,
 PT preventing and/or treating disorders, such as cancer, glomerulonephritis,
 PT rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
 XX
 PF Example 27; Page 218; 265pp; English.
 XX
 CC The invention relates to novel Drosophila species DNA sequences and their
 CC encoded proteins with their corresponding human homologues. The proteins
 CC or their encoding polynucleotides are useful in a method of prevention,
 CC treatment or diagnosis of a disease in an individual, and used to
 CC identify a substance capable of binding to the polypeptide or modulating
 CC the function of the polypeptide comprising incubating the polypeptide
 CC with a candidate substance and determining whether the substance binds to
 CC the polypeptide. The compositions are administered to an individual in
 CC need of such treatment. The method of diagnosis, in which the presence or
 CC absence of a polynucleotide is detected in a biological sample, comprises
 CC brining the biological sample containing the nucleic acid such as DNA or
 CC RNA into contact with a probe comprising a fragment of at least 15
 CC nucleotides of the polynucleotide, and detecting any duplex formed
 CC between the probe and nucleic acid in the sample. The method also
 CC comprises providing an antibody capable of binding to the polypeptide,
 CC incubating a biological sample with the antibody to allow the formation
 CC of an antibody-antigen complex, and determining whether antibody-antigen
 CC complex comprising the antibody is formed. The disease comprises a
 CC proliferative disease such as cancer. The antibody or identified
 CC substance is also useful in inhibiting the function of a polypeptide

CC and/or regulating a cell division cycle function. The diseases also
 CC include cardiovascular disorders, autoimmune diseases such as
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as
 CC malaria, emphysema and alopecia. This sequence represents a human homolog
 CC for one of the Drosophila proteins of the invention.
 XX
 SQ Sequence 420 AA;
 Query Match 97.3%; Score 2024; DB 7; Length 420;
 Best Local Similarity 100.0%; Pred. No. 5e-210;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 MSGRPRTTFAESCKDVQPSAFSGSMKVSRDKDGSKVTTVATPGQDPDPQEVSYDTK 70
 Db 1 MSGRPRTTFAESCKDVQPSAFSGSMKVSRDKDGSKVTTVATPGQDPDPQEVSYDTK 60
 Qy 71 VINGSGFVVYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYS 130
 Db 61 VINGSGFVVYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLHCNIVRLRYFFYS 120
 Qy 131 EKDEVYLNLDYVPETVVRVARYHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 190
 Db 121 EKDEVYLNLDYVPETVVRVARYHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 180
 Qy 191 DIKPNLLDPPFAVLKLCDFGSAKQLVKRGEPNVSYCSRYRPAELIFGATDYTSIDV 250
 Db 181 DIKPNLLDPPFAVLKLCDFGSAKQLVKRGEPNVSYCSRYRPAELIFGATDYTSIDV 240
 Qy 251 WSAGCVLAELLGQIPFGDGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
 Db 241 WSAGCVLAELLGQIPFGDGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 300
 Qy 311 WTKVFRPTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
 Db 301 WTKVFRPTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 6
 ADH09637
 ID ADH09637 standard; protein; 420 AA.
 XX
 AC ADH09637;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human host factor protein, SEQ ID No 165.
 XX
 KW antiviral; host factor; retrovirus; HIV; human.
 OS Homo sapiens.
 XX
 PN W02003094847-A2.
 XX
 PD 20-NOV-2003.
 XX
 PF 07-MAY-2003; 2003WO-US014382.
 XX
 PR 07-MAY-2002; 2002US-0378711P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Devine SE;
 XX
 DR WPI; 2004-011998/01.
 XX
 PT Identifying an antiviral compound useful for treating HIV comprises
 PT exposing a cell that expresses a host factor to a candidate compound to
 PT identify an agent that inhibits the expression or activity of the host

PT factor.
XX Claim 13; SEQ ID NO 165; 141pp; English.
XX
XX
CC The invention relates to a novel method for identifying an antiviral
CC compound. The novel method comprises exposing a cell that expresses a
CC host factor to a candidate compound to identify an agent that inhibits
CC the expression or activity of the host factor. The novel method involves
CC identifying an antiviral compound, comprising exposing a first cell that
CC expresses a host factor to a candidate compound, determining whether the
CC candidate compound inhibits the expression or activity of the host factor
CC in the first cell, where a candidate compound that inhibits the
CC expression or activity of the host factor in the first cell is a
CC potential antiviral compound, exposing a second cell to the potential
CC antiviral compound and a retrovirus, and determining whether the compound
CC inhibits the ability of the retrovirus to infect or replicate within the
CC second cell, where a potential antiviral compound that inhibits the
CC ability of the retrovirus to infect the second cell is an antiviral
CC compound. The method is useful in identifying antiviral agents, including
CC those that are effective against retroviruses, such as HIV. This sequence
CC represents a human host factor protein used in the antiviral
CC identification method of the invention.
XX
XX
SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 5e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTFAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQDPDRPQSVYTDK 70
DB 1 MSGRPRTTFAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQDPDRPQSVYTDK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120

QY 131 EKDEVYLNVLVDYVPETVYRVARHYSRKQTLPIVYVKLYMYQLFRSLAYIHSFGIC 190
DB 121 EKDEVYLNVLVDYVPETVYRVARHYSRKQTLPIVYVKLYMYQLFRSLAYIHSFGIC 180

QY 191 DIKPNLLDPPDPAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFGATDYSIDV 250
DB 181 DIKPNLLDPPDPAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQIPFGDSGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310
DB 241 WSAGCVLAELLGQIPFGDSGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPRTPEAIALCSRLLVTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEAIALCSRLLVTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

QY 371 NFTQELSSNPPLATILIPPHARI 394
DB 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 7
AD40191
ID ADR40191 standard; protein; 420 AA.
XX
AC ADR40191;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human glycogen synthase kinase 3 beta (GSK3beta) (1521) protein.
XX
KW haematological; cytostatic; erythroid; anaemia; erythrocytosis;
KW bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;
KW T-cells; neutropenia; gene therapy; human;
KW glycogen synthase kinase 3 beta; GSK3beta; enzyme.
XX

OS Homo sapiens.
XX WO2004072242-A2.
XX
XX 26-AUG-2004.
XX
XX 05-FEB-2004; 2004WO-US003417.
XX
XX 05-FEB-2003; 2003US-0445241P.
XX 18-FEB-2003; 2003US-0448389P.
XX 20-MAR-2003; 2003US-0456320P.
XX 03-APR-2003; 2003US-0460279P.
XX 28-APR-2003; 2003US-0465924P.
XX 13-MAY-2003; 2003US-0470052P.
XX 26-AUG-2003; 2003US-0498106P.
XX 04-SEP-2003; 2003US-0500179P.
XX 15-SEP-2003; 2003US-0502909P.
XX 10-OCT-2003; 2003US-0510351P.
XX 17-OCT-2003; 2003US-0512380P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Kelly LM, Carroll JM, Farlow D, Healy A;
XX
XX WPI; 2004-625850/60.
XX N-PSDB; ADR40190.
XX
XX Identifying a compound capable of treating a hematological disorder
XX comprises combining a compound to be tested with a polypeptide related
XX with the disorder under conditions suitable for binding of the test
XX compound to the polypeptide.
XX
XX Claim 1; SEQ ID NO 72; 321pp; English.
XX
XX The invention relates to a novel method for identifying a compound
XX capable of treating a haematological disorder which comprises combining a
XX compound to be tested with a specific polypeptide under conditions
XX suitable for binding of the test compound to the polypeptide. The method
XX of the invention has haematological and cytostatic applications and may
XX be useful for identifying compounds for treating a haematological
XX disorder associated with erythroid cells e.g. anaemia and erythrocytosis,
XX bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and
XX thrombosis or B-cells and T-cells e.g. neutropenia. The compounds
XX identified may be utilised during gene therapy procedures. The current
XX sequence is that of a human haematological disorder-related protein of
XX the invention.
XX
XX Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 5e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTFAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQDPDRPQSVYTDK 70
DB 1 MSGRPRTTFAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQDPDRPQSVYTDK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYS 120

QY 131 EKDEVYLNVLVDYVPETVYRVARHYSRKQTLPIVYVKLYMYQLFRSLAYIHSFGIC 190
DB 121 EKDEVYLNVLVDYVPETVYRVARHYSRKQTLPIVYVKLYMYQLFRSLAYIHSFGIC 180

QY 191 DIKPNLLDPPDPAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFGATDYSIDV 250
DB 181 DIKPNLLDPPDPAVLKLCDFGSAKQIVRGEPNVSYICSYRYRAPELIFGATDYSIDV 240

QY 251 WSAGCVLAELLGQIPFGDSGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 310
DB 241 WSAGCVLAELLGQIPFGDSGVQDLVEIIVKLGTPTRQIREMNPNTYEFKFPQIKAH 300

QY 311 WTKVFRPTTPEAIALCSRLLEYTPARTLPLECAHSPFDELDRDNNVHPNGRDTPALF 370
 DB 301 WTKVFRPTTPEAIALCSRLLEYTPARTLPLECAHSPFDELDRDNNVHPNGRDTPALF 360
 QY 371 NFFTQELSSNPPLATILIPPHARI 394
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 8
 ADS92965
 ID ADS92965 standard; protein; 420 AA.
 XX
 AC ADS92965;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Glycogen synthase kinase 3 beta.
 XX
 KW cytostatic; gene therapy; human;
 KW branching morphogenesis modulating agent; MBM agent.
 XX
 OS Homo sapiens.
 XX
 PN W02004037990-A2.
 XX
 PD 06-MAY-2004.
 XX
 XX 22-OCT-2003; 2003MO-US033549.
 PF
 PR 23-OCT-2002; 2002US-0420554P.
 PR 30-DEC-2002; 2002US-0436941P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Plowman GD, Karim FD, Swimmer C, Habeck HA, Koblizek TI;
 PI Schulte-Werker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
 PI Odenthal JH, Scheel JK, Will TT, Jin Y, Bjertke LM, Hal B;
 PI Adamkewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
 PI Nicoll M;
 DR WPI; 2004-365506/34.
 DR N-PSDB; ADS92934.
 XX
 PT Identifying a candidate branching morphogenesis modulating agent for
 PT treating cancer comprises contacting the assay system comprising a MBM
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-
 PT biased activity.
 XX
 PS Example 3; SEQ ID NO 36; 179pp; English.
 XX
 CC The invention describes a method of identifying a candidate branching
 CC morphogenesis modulating (MBM) agent. The method comprises: providing an
 CC assay system comprising a MBM polypeptide or nucleic acid; contacting the
 CC assay system with a test agent under conditions where the system provides
 CC a reference activity, except for the presence of the test agent; and
 CC detecting a test agent-biased activity of the assay system, where a
 CC difference between the test agent-biased activity and the reference
 CC activity identifies the test agent as a candidate branching morphogenesis
 CC modulating agent. Also described are: a method of modulating branching
 CC morphogenesis in a mammalian cell; and a method for diagnosing a disease
 CC in a patient. The method is useful in identifying a candidate branching
 CC morphogenesis modulating agent for preparing a composition for diagnosing
 CC or treating cancer. This is the amino acid sequence of a human branching
 CC morphogenesis modulating (MBM) protein.
 XX
 SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;
 Best Local Similarity 100.0%; Pred. No. 5e-210;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 11 MSGRPTTSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQDPDRPQEVSYDTDK 70

DB 1 MSGRPTTSPAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQDPDRPQEVSYDTDK 60
 QY 71 VTGNGSFGVYQAKLCSGELVAIKVLQDQKPNRELOIMRKLHCHNIVRLRYFFYSYG 130
 DB 61 VTGNGSFGVYQAKLCSGELVAIKVLQDQKPNRELOIMRKLHCHNIVRLRYFFYSYG 120
 QY 131 EKKDEVYANLVDYVPETVYVARHYHSAKQTLPTVYVLYMYQLFRSLAYIHSFGICHR 190
 DB 121 EKKDEVYANLVDYVPETVYVARHYHSAKQTLPTVYVLYMYQLFRSLAYIHSFGICHR 180
 QY 191 DIKPNLLDPPDTAVLKLCDGSAKQVVRGEPNVSYICSRYYRAPERLIFGATDYSIDV 250
 DB 181 DIKPNLLDPPDTAVLKLCDGSAKQVVRGEPNVSYICSRYYRAPERLIFGATDYSIDV 240
 QY 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIRRMNPNYTFKFPQKAHP 310
 DB 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKLGTPTRQIRRMNPNYTFKFPQKAHP 300
 QY 311 WTKVFRPTTPEAIALCSRLLEYTPARTLPLECAHSPFDELDRDNNVHPNGRDTPALF 370
 DB 301 WTKVFRPTTPEAIALCSRLLEYTPARTLPLECAHSPFDELDRDNNVHPNGRDTPALF 360
 QY 371 NFFTQELSSNPPLATILIPPHARI 394
 DB 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 9
 ADT92555
 ID ADT92555 standard; protein; 420 AA.
 XX
 AC ADT92555;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human glycogen synthase kinase-3-related protein - SEQ ID 1.
 XX
 KW neuroregenerative drug; glycogen synthase kinase-3; GSK-3;
 KW neurological disease; Parkinson's disease; Alzheimer's disease;
 KW Down's syndrome; cerebrovascular accident; stroke; spinal injury;
 KW Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis;
 KW epilepsy; anxiety disorder; schizophrenia; depression;
 KW manic-depressive psychosis.
 XX
 OS Homo sapiens.
 XX
 PN W02004091663-A1.
 XX
 PD 28-OCT-2004.
 XX
 PF 16-APR-2004; 2004MO-JP005503.
 XX
 PR 18-APR-2003; 2003JP-00114579.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Morishita T, Sakurada K, Suzuki K, Ikeda S;
 DR WPI; 2004-784511/77.
 DR N-PSDB; ADT92556.
 XX
 PT Neuroregenerative drug for treating neurological disease e.g. Parkinson's
 PT disease, Alzheimer's disease and Down's syndrome, contains substance
 PT which inhibits activity of glycogen synthase kinase-3 as active
 PT ingredient.
 XX
 PS Disclosure; SEQ ID NO 1; 115pp; Japanese.
 XX
 CC The invention comprises a neuroregenerative drug that inhibits the
 CC activity of glycogen synthase kinase-3 (GSK-3). The neuroregenerative
 CC drug of the invention is useful for treating neurological disease, such
 CC as: Parkinson's disease, Alzheimer's disease, Down's syndrome,

CC cerebrovascular accident, stroke, spinal injury, Huntington's chorea,
 CC multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, anxiety
 CC disorder, schizophrenia, depression and manic-depressive psychosis. The
 CC present human protein is used in the exemplification of the invention.
 XX
 SQ Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;
 Best Local Similarity 100.0%; Pred. No. 5e-210;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 70
 Db 1 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 60
 Qy 71 VINGSGVGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFSYSSG 130
 Db 61 VINGSGVGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFSYSSG 120
 Qy 131 EKXDEVYLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 190
 Db 121 EKXDEVYLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 180
 Qy 191 DIKPNLLDPTAVLKCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
 Db 181 DIKPNLLDPTAVLKCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
 Qy 251 WSAGCVLAELLGQPIPPGDSGVQDLVEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
 Db 241 WSAGCVLAELLGQPIPPGDSGVQDLVEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 300
 Qy 311 WTKVFRPTPEALCSRLLYPTPTARLTPLCAHSAHFFDELDPNVKHPNGRDTPALF 370
 Db 301 WTKVFRPTPEALCSRLLYPTPTARLTPLCAHSAHFFDELDPNVKHPNGRDTPALF 360
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 10
 ADR06333
 ID ADR06333 standard; protein; 414 AA.
 XX
 AC ADR06333;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE p38-alpha kinase, SEQ ID 31.
 XX
 KW Switch control ligand; switch control pocket;
 KW protein activity modulation; human; p38-alpha kinase; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2004061084-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 26-DEC-2003; 2003WO-US041450.
 XX
 PR 31-DEC-2002; 2002US-0437304P.
 PR 31-DEC-2002; 2002US-0437403P.
 PR 31-DEC-2002; 2002US-0437415P.
 PR 31-DEC-2002; 2002US-0437487P.
 PR 18-APR-2003; 2003US-0463804P.
 PR 24-DEC-2003; 53US-00463804.
 XX
 PA (DECI-) DECIPHERA PHARM INC.
 XX
 PI Flynn DL, Petrillo PA;
 XX
 XX WPI; 2004-534376/51.
 DR

XX Identifying molecules that interact with specific naturally occurring
 PT proteins for modulating protein activity, comprises identifying molecules
 PT that bind with the protein at the region of the pocket to regulate
 PT activity of the protein.
 XX
 PS Disclosure; SEQ ID NO 31; 204pp; English.
 XX
 CC The present invention relates to a method for identifying molecules,
 CC which interact with proteins e.g. enzymes, receptors, or signaling
 CC proteins, in order to regulate the activity of the proteins. The method
 CC comprises: identifying a switch control ligand forming a part of the
 CC protein; identifying a switch control pocket forming a part of the
 CC protein and which interacts with the switch control ligand, where the
 CC ligand interacting in vivo with the pocket to regulate the conformation
 CC and biological activity of the protein so that the protein will assume a
 CC first conformation and a first biological activity upon the ligand-pocket
 CC interaction, and will assume a second, different conformation and a
 CC biological activity in the absence of the ligand-pocket interaction;
 CC providing respective samples of the protein in the first and second
 CC conformations; and screening at least one of the samples against one or
 CC more candidate molecules by contacting the molecules and one sample, and
 CC identifying small molecules which bind with the protein at the region of
 CC the pocket in order to regulate the activity of the protein. The method
 CC is useful for modulating protein activity and for the identification of
 CC new pharmacological compounds and for treatment modalities. The present
 CC sequence is p38-alpha kinase for which a switch control ligand was
 CC produced.
 XX
 SQ Sequence 414 AA;

Query Match 96.7%; Score 2013; DB 8; Length 414;
 Best Local Similarity 99.7%; Pred. No. 7.6e-209;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 70
 Db 1 MSGRPRTTSAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYDTK 60
 Qy 71 VINGSGVGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFSYSSG 130
 Db 61 VINGSGVGVYQAKLDCSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFSYSSG 120
 Qy 131 EKXDEVYLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 190
 Db 121 EKXDEVYLVLDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFRSLAYIHSGICH 180
 Qy 191 DIKPNLLDPTAVLKCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
 Db 181 DIKPNLLDPTAVLKCDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
 Qy 251 WSAGCVLAELLGQPIPPGDSGVQDLVEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
 Db 241 WSAGCVLAELLGQPIPPGDSGVQDLVEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 300
 Qy 311 WTKVFRPTPEALCSRLLYPTPTARLTPLCAHSAHFFDELDPNVKHPNGRDTPALF 370
 Db 301 WTKVFRPTPEALCSRLLYPTPTARLTPLCAHSAHFFDELDPNVKHPNGRDTPALF 360
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 11
 AAR61327
 ID AAR61327 standard; protein; 420 AA.
 XX
 AC AAR61327;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-APR-1995 (first entry)
 XX

DE Tau-protein kinase I (TPK-I), Alzheimer's disease.
XX
XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease.
XX
OS Rattus rattus.
XX
XX EP616032-A2.
XX
XX 21-SEP-1994.
XX
XX 01-MAR-1994; 94EP-00103057.
XX
XX 02-MAR-1993; 93JP-00041160.
XX
XX 22-MAR-1993; 93JP-00085143.
XX
XX 02-AUG-1993; 93JP-00191246.
XX
XX (MITU) MITSUBISHI KASEI CORP.
XX
XX (MITU) MITSUBISHI CHEM CORP.
XX
XX Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A;
XX
XX Sato S;
XX
XX WPI; 1994-287181/36.
XX
XX N-PSDB; AAQ67459.
XX
XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-
XX
XX protein providing means for prevention and treatment of Alzheimer's
XX
XX disease.
XX
XX Claim 4; Page 18; 30pp; English.
XX
XX AAQ67459 codes for a newly isolated tau-protein kinase I enzyme (TPK-1),
XX
XX shown in AAR61327 (compare to human AAR61326). The cDNA was cloned from a
XX
XX rat fetus brain cDNA library, and was expressed in insect cells. TPK-I
XX
XX acts specifically on tau-protein, which is thought to be involved in
XX
XX Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped
XX
XX that the characterisation of TPK-I may lead to development of new agents
XX
XX for the prevention and therapy of these diseases. (Updated on 25-MAR-2003
XX
XX to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX SQ Sequence 420 AA;
XX
XX Query Match 96.7%; Score 2013; DB 2; Length 420;
XX
XX Best Local Similarity 99.7%; Pred. No. 7.8e-209;
XX
XX Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 11 MSGRPRTTSPAESCKPVQQPSPAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
XX
XX 1 MSGRPRTTSPAESCKPVQQPSPAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
XX
XX 71 VINGSGGVVYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130
XX
XX 61 VINGSGGVVYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120
XX
XX 131 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFRSLAYIHSGFCHR 190
XX
XX 121 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFRSLAYIHSGFCHR 180
XX
XX 191 DIKQNLDDPDATVAKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 250
XX
XX 181 DIKQNLDDPDATVAKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 240
XX
XX 251 WSAGCVLAELLGQPIFPFGSGVDQVLEIKVLGTPTRQIRENNPNYTFKFPQIIKAHP 310
XX
XX 241 WSAGCVLAELLGQPIFPFGSGVDQVLEIKVLGTPTRQIRENNPNYTFKFPQIIKAHP 300
XX
XX 311 WTKVFRPRTPEALCSRLLVPTARLTLECAHSFPDELDPNVKHPNGRDTPALF 370
XX
XX 301 WTKVFRPRTPEALCSRLLVPTARLTLECAHSFPDELDPNVKHPNGRDTPALF 360
XX
XX 371 NFFTQELSSNPPLATILIPPHARI 394
XX
XX 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 12
ABB77875
ID ABB77875 standard; peptide; 420 AA.
XX
XX ABB77875;
XX
XX 27-SEP-2002 (first entry)
XX
XX Amino acid sequence of glycogen synthase kinase 3 isoform beta.
XX
XX Glycogen synthase kinase 3 beta; GSK3beta; T-cell lymphoma; stroke;
XX
XX Type II diabetes mellitus; obesity; neurodegenerative disorder; cancer;
XX
XX Alzheimer's disease; mood disorder; depression; schizophrenia;
XX
XX cyclin-dependent kinase 2; substrate; protein coordinate data.
XX
XX Homo sapiens.
XX
XX WO20020254-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-GB005632.
XX
XX 18-DEC-2000; 2000GB-00030846.
XX
XX 14-AUG-2001; 2001GB-00019796.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX Bax B, Brown M, Reith A;
XX
XX WPI; 2002-519885/55.
XX
XX Novel crystal structures comprising glycogen synthase kinase (GSK)-3 beta
XX
XX protein or crystal structure comprising a GSK-3 beta: frequently
XX
XX rearranged in advanced T-cell lymphomas (PRAT)-tide complex in
XX
XX crystalline form.
XX
XX Claim 6; Page 23; 327pp; English.
XX
XX The specification describes the structure of glycogen synthase kinase
XX
XX (GSK)3beta protein in crystalline form. GSK3beta is frequently rearranged
XX
XX in advanced T-cell lymphomas. The crystalline structure of GSK3beta is
XX
XX useful in the design or selection of potential inhibitors and/or
XX
XX activators of GSK3beta kinase activity. Such inhibitors and activators
XX
XX are useful for treating Type II diabetes mellitus, obesity,
XX
XX neurodegenerative disorders such as Alzheimer's disease, stroke and mood
XX
XX disorders such as bipolar and unipolar depression, schizophrenia, cancer,
XX
XX in humans. Because GSK3beta may crystallize in more than one crystal
XX
XX form, the structure coordinates of GSK3 or its portions are particularly
XX
XX useful to solve the structure of other crystal forms of GSK3. They may
XX
XX also be used to solve the structure of GSK3 mutants, GSK3 co-complexes,
XX
XX or of the crystalline form of any other protein, particularly kinases
XX
XX with significant amino acid sequence homology to any functional domain of
XX
XX GSK3. The present sequence represents the beta isoform of GSK3, GSK3beta
XX
XX SQ Sequence 420 AA;
XX
XX Query Match 96.7%; Score 2013; DB 5; Length 420;
XX
XX Best Local Similarity 99.7%; Pred. No. 7.8e-209;
XX
XX Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 11 MSGRPRTTSPAESCKPVQQPSPAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
XX
XX 1 MSGRPRTTSPAESCKPVQQPSPAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
XX
XX 71 VINGSGGVVYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130
XX
XX 61 VINGSGGVVYQAKLDSGELVAIKKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120
XX
XX 131 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFRSLAYIHSGFCHR 190
XX
XX 121 EKKDEVYLVLDVVPETVYRVARHYSRAKQTLPIVYVYKLYMYQLFRSLAYIHSGFCHR 180
XX
XX 191 DIKQNLDDPDATVAKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 250
XX
XX 181 DIKQNLDDPDATVAKLDFGSAKQVLRGPNVSYICSRYPAPELIFGATDYSIDV 240
XX
XX 251 WSAGCVLAELLGQPIFPFGSGVDQVLEIKVLGTPTRQIRENNPNYTFKFPQIIKAHP 310
XX
XX 241 WSAGCVLAELLGQPIFPFGSGVDQVLEIKVLGTPTRQIRENNPNYTFKFPQIIKAHP 300
XX
XX 311 WTKVFRPRTPEALCSRLLVPTARLTLECAHSFPDELDPNVKHPNGRDTPALF 370
XX
XX 301 WTKVFRPRTPEALCSRLLVPTARLTLECAHSFPDELDPNVKHPNGRDTPALF 360
XX
XX 371 NFFTQELSSNPPLATILIPPHARI 394
XX
XX 361 NFFTQELSSNPPLATILIPPHARI 384

Db 121 EKKDEVYLVLDVVPETVVRVARYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGFICHR 180
 Qy 191 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
 Db 181 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
 Qy 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
 Db 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 300
 Qy 311 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGRDTPALF 370
 Db 301 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGRDTPALF 360
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 13
 ABP70714
 ID ABP70714 standard; protein; 420 AA.
 XX
 AC ABP70714;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Human glycogen synthase kinase-3 beta.
 XX
 KW Human; enzyme; glycogen synthase kinase-3 beta; protein co-ordinate data;
 KW neurotropic; neuroprotective; neuroleptic; antidiabetic; immunosuppressive;
 KW antiinflammatory; cardiovascular; antiallergic; antiasthmatic;
 KW antiparkinsonian; anticonvulsant; dermatological; vasotrophic; GSK-3;
 KW schizophrenia; Alzheimer's disease; diabetes; autoimmune disease;
 KW inflammatory disease; metabolic; neurological; neurodegenerative;
 KW cardiovascular disease; allergy; asthma; Huntington's disease;
 KW Parkinson's disease; AIDS-related dementia; Lou Gehrig's disease;
 KW amyotrophic lateral sclerosis; multiple sclerosis; kinase;
 KW cardiomyocyte hypertrophy; reperfusion; ischaemia; baldness.
 XX
 OS Homo sapiens.
 XX
 PN WO200288078-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 29-APR-2002; 2002WO-US013511.
 XX
 PR 30-APR-2001; 2001US-0287366P.
 PR 08-JUN-2001; 2001US-0297094P.
 PR 27-FEB-2002; 2002US-0361899P.
 XX
 PA (VERT-) VERTEX PHARM INC.
 XX
 PI Ter Haar E, Swenson L, Green J, Arnost MJ;
 XX
 DR WPI; 2003-247844/24.
 XX
 PT New pyrazolo(3,4-c)pyridazine derivatives are glucagon synthase kinase-3
 inhibitors useful for treating e.g. schizophrenia, Alzheimer's disease, and
 diabetes, autoimmune diseases, allergy, asthma, multiple sclerosis, and
 baldness.
 XX
 PS Claim 36; Page 777-778; 778pp; English.
 XX
 CC The present invention relates to novel pyrazolo(3,4-c)pyridazine
 derivatives, which have glucagon synthase kinase-3 (GSK-3) inhibitory
 activity. The derivatives are useful for inhibiting beta-catenin
 phosphorylation and hyperphosphorylated Tau protein production in a
 patient and GSK-3 activity in a patient or in a biological sample. The
 derivatives are also useful for treating schizophrenia, Alzheimer's
 disease, diabetes, autoimmune diseases, inflammatory diseases, metabolic,
 neurological and neurodegenerative diseases, cardiovascular diseases,

CC allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related
 CC dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple
 CC sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness.
 CC The present sequence is human GSK-3 beta, used to illustrate the
 CC invention. GSK-3 beta is a serine/threonine protein kinase
 XX
 SQ Sequence 420 AA;
 Query Match 96.7%; Score 2013; DB 6; Length 420;
 Best Local Similarity 99.7%; Pred. No. 7.8e-209;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 11 MSGRPRTTSAEACKPVQPSAFSGSMKVSQKSGKVTTVVATPGQGPDRPQEVSYDTK 70
 Db 1 MSGRPRTTSAEACKPVQPSAFSGSMKVSQKSGKVTTVVATPGQGPDRPQEVSYDTK 60
 Qy 71 VINGSGFVVYQAKLCDSGELVAIKVLODKRFKNRELOIMRKLDHCNIVLRVFFYSYG 130
 Db 61 VINGSGFVVYQAKLCDSGELVAIKVLODKRFKNRELOIMRKLDHCNIVLRVFFYSYG 120
 Qy 131 EKKDEVYLVLDVVPETVVRVARYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGFICHR 190
 Db 121 EKKDEVYLVLDVVPETVVRVARYHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGFICHR 180
 Qy 191 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
 Db 181 DIKPNLLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
 Qy 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
 Db 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKVLGTPTRQIREMNPNTYEFKFPQIKAH 300
 Qy 311 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGRDTPALF 370
 Db 301 WTKVFRPTPEALALCSRLLEYTPPTARLTPLECAHSPFDELDPNVKHPNGRDTPALF 360
 Qy 371 NFFTQELSSNPPLATILIPPHARI 394
 Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 14
 ABR44293
 ID ABR44293 standard; protein; 420 AA.
 XX
 AC ABR44293;
 XX
 DT 18-AUG-2003 (first entry)
 XX
 DE Human glycogen synthase kinase-3 (GSK3)beta polypeptide.
 XX
 KW GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
 KW vulnary; antiarteriosclerotic; GSK3beta; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO2003038037-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 23-OCT-2002; 2002WO-US033909.
 XX
 PR 29-OCT-2001; 2001US-0350160P.
 PR 13-NOV-2001; 2001US-0337905P.
 XX
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
 XX
 PI Walsh K;
 XX
 DR WPI; 2003-482140/45.
 XX
 PT Modulating angiogenesis, useful for treating hyperlipidemia, comprises
 administering an angiogenesis inhibitor/promoter, such as an

PT active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3
PT activator/inhibitor.
PS Disclosure; Page 97-99; 115pp; English.
XX
XX The invention relates to inhibiting/enhancing angiogenesis. The method
XX involves administering to a subject needing the treatment, an
CC angiogenesis inhibitor/promoter, such as an active/inactive glycogen
CC synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,
CC where the angiogenesis modulator is administered to inhibit/enhance
CC angiogenesis in a subject. The methods are useful for treating a
CC condition associated with increased apoptotic cell death of vascular
CC endothelial cells, where the condition is characterized by lesion of
CC blood vessel wall, such as hyperlipidemia, also in the treatment of
CC myocardial infarction and in the promotion of wound healing. The present
CC sequence represents a human GSK3beta polypeptide (GenBank Accession No.
CC P49841)
XX
SQ Sequence 420 AA;

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.8e-209;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60

Qy 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 120

Qy 131 EKXDEVYLNLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 190
Db 121 EKXDEVYLNLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 180

Qy 191 DIKPQNLLDPDTAVLKCDPFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLLDPDTAVLKCDPFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240

Qy 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 15
ADD68742
ID ADD68742 standard; protein; 420 AA.
XX
XX ADD68742;
XX
XX 15-JAN-2004 (first entry)
XX
XX Rat tau phosphorylation-related protein.
XX
XX tau; phosphoenzyme I; Alzheimer's disease; senile dementia;
XX serine-threonine phosphorylation; rat.
XX
XX Rattus sp.
XX
XX JP2002335983-A.
XX
XX 26-NOV-2002.
XX
XX 03-JUL-1992; 2002JP-00129146.

XX
PR 03-JUL-1992; 92JP-00177241.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
XX WPI; 2003-460769/44.
XX N-PSDB; ADD68695.
XX
XX Phosphorylation of tau protein.
XX
XX Disclosure; Page 11-13; 29pp; Japanese.
XX
XX The invention relates to a novel method for the phosphorylation of tau
XX protein in which tau protein or its partial peptide is phosphorylated by
XX the action of phosphoenzyme I, a serine-threonine phosphatase. The
XX method of the invention may be used for elucidation of the cause of
XX Alzheimer's disease and Alzheimer type senile dementia. The current
XX sequence is that of the rat tau phosphorylation-related protein of the
XX invention.
XX
SQ Sequence 420 AA;

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.8e-209;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSAESCKPVQPSAFGSMKVS RDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60

Qy 71 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VINGSGFVVYQAKLDCSGELVAIKVLDQKRFKNRELOIMRKLDHCNIVRLRYFFYSYG 120

Qy 131 EKXDEVYLNLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 190
Db 121 EKXDEVYLNLDVVPETVVRVARHYSRAKQTLPIVIVVKLYMYQLFRSLAYIHSGICHR 180

Qy 191 DIKPQNLLDPDTAVLKCDPFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 250
Db 181 DIKPQNLLDPDTAVLKCDPFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYTSSIDV 240

Qy 251 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIPPGDSGVDQVLEIIVKVLGTPTREQIREMNPNTYEFKFPQIKAH 300

Qy 311 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEAIALCSRLLVYPTTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

Search completed: September 15, 2006, 17:07:03
Job time : 199 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 15, 2006, 17:07:20 ; Search time 40 Seconds
(without alignments)
947.735 Million cell updates/sec

Title: US-10-733-816-2
Perfect score: 2081
Sequence: 1 MEYMPMEGGMGSRPRTTGF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2024	97.3	420	1 S53324	glycogen synthase
2	2010	96.6	420	1 TVRTRKB	tau-protein kinase
3	1931	92.8	420	2 I51425	intracellular kina
4	1923	92.4	420	2 I51425	glycogen synthase
5	1607	77.2	483	1 TVRTRKA	protein kinase (EC
6	1590.5	76.4	575	2 S35327	protein kinase sgg
7	1542.5	74.1	733	2 S10932	probable protein k
8	1542.5	74.1	1067	2 S35423	protein kinase sgg
9	1342.5	64.5	362	2 T26520	hypothetical prote
10	1296	62.3	409	2 S51105	shaggy protein kin
11	1275.5	61.3	471	2 T03601	shaggy protein kin
12	1273.5	61.2	471	1 T02297	shaggy protein kin
13	1265	60.8	408	2 T48637	protein kinase MSK
14	1258	60.5	472	1 T01236	serine/threonine-s
15	1256	60.4	412	1 S37642	protein kinase MSK
16	1249	60.0	403	2 T03777	probable shaggy-li
17	1249	60.0	431	2 S51106	shaggy protein kin
18	1247.5	59.9	469	1 T02256	shaggy protein kin
19	1246	59.9	409	1 S41597	protein kinase ASK
20	1245	59.8	412	2 T71266	shaggy-like protei
21	1244	59.8	411	1 S37643	protein kinase MSK
22	1239	59.5	409	2 S52095	tau-protein kinase
23	1234	59.3	380	2 T04863	shaggy-like protei
24	1233	59.3	412	2 A84715	probable shaggy-li
25	1232	59.2	405	1 S41596	protein kinase ASK
26	1232	59.2	407	2 S77922	shaggy-like protei
27	1229.5	59.1	420	2 A96613	probable glycogen
28	1229.5	59.1	469	1 T02254	shaggy protein kin
29	1228.5	59.0	447	2 F86232	hypothetical prote

protein kinase MSK
shaggy-like protei
protein kinase Atk
hypothetical prote
protein kinase (EC
shaggy-like kinase
protein kinase sgp
protein kinase skp
serine-threonine p
probable protein k
glycogen synthase
hypothetical prote
protein kinase RIM
MKI protein - yea
probable serine/th
hypothetical prote

30 1226 58.9 411 1 S37644
31 1226 58.9 468 2 T08139
32 1220 58.6 421 2 S51938
33 1208 58.0 447 2 T01756
34 1178 56.6 468 2 A55476
35 1158 55.6 431 2 T47908
36 1156.5 55.6 387 2 T37758
37 1109.5 53.3 354 2 T45138
38 996 47.9 381 2 T40746
39 996 47.9 390 2 T43008
40 978.5 47.0 452 2 T18457
41 940.5 45.2 354 2 F90121
42 940 45.2 370 2 A56347
43 873.5 42.0 501 2 S67615
44 792 38.1 211 2 T04119
45 735.5 35.3 367 2 T19937

ALIGNMENTS

glycogen synthase kinase 3 beta (EC 2.7.1.1) - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S53324
R;Stambolic, V.; Woodgett, J.R.
Biochem. J. 303, 701-704, 1994
A;Title: Mitogen inactivation of glycogen synthase kinase-3-beta in intact cells via ser
A;Reference number: S53324; MUID:95071278; PMID:7980435
A;Accession: S53324
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-420 <STA>
A;Cross-references: UNIPROT:P49841; UNIPARC:UPI000004B93D; EMBL:L33801; NID:G529236; PID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Comment: This enzyme is inhibited by phosphorylation of serine 9 by p70 S6 kinase (see
C;Genetics:
A;Gene: GDB:GSK3B
A;Cross-references: GDB:6108057
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase
F;54-315/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;9/Binding site: phosphate (Ser) (covalent) (by ribosomal protein S6 kinase) #status ex
F;85/Active site: Lys #status predicted

Query Match	97.3%	Score	2024	DB	1	Length	420
Best Local Similarity	100.0%	Pred. No.	2.6e-89				
Matches	384	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	11	MSGRPRTTSFAESCCKPVQQPSAFSGMKVSRDKGSKVTTVVATPGQCPDRPQEVSYDTK	70				
Db	1	MSGRPRTTSFAESCCKPVQQPSAFSGMKVSRDKGSKVTTVVATPGQCPDRPQEVSYDTK	60				
Qy	71	VINGSGFVVYQAKLDCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCHNIVLRYFFYS	130				
Db	61	VINGSGFVVYQAKLDCDSGELVAIKKVLQDKRFKNRELQIMRKLDHCHNIVLRYFFYS	120				
Qy	131	EKDEVYLNVLVDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFSLAYIHSFGICHR	190				
Db	121	EKDEVYLNVLVDVYPETVYRVARHYSRAKQTLPIVYVKLYMYQLFSLAYIHSFGICHR	180				
Qy	191	DIRPQNLLDPDTAVLKLCDFGSAKQLVRGPNVSYICSRYYRAPELIFGATDVTSSIDV	250				
Db	181	DIRPQNLLDPDTAVLKLCDFGSAKQLVRGPNVSYICSRYYRAPELIFGATDVTSSIDV	240				
Qy	251	WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTPFREQIREMNPNTYEFKFPQIKAH	310				
Db	241	WSAGCVLAELLGQPIFPDGSVDQVLEIIVKLGTPFREQIREMNPNTYEFKFPQIKAH	300				
Qy	311	WTKVFRPRTPEALCSRLLEYPPTARLTIPLECAHSAFDELDPNVKHPNGRDTALF	370				

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Db 301 WTKVFRPTTPEALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 2
TVRTKB
A;Title: tau-protein kinase (EC 2.7.1.135) I - rat
N;Alternate names: factor A; Glycogen synthase kinase 3 beta; protein kinase GSK-3-beta;
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S14708; S36729
R;Woodgett, J.R.
EMBO J. 9, 2431-2438, 1990
A;Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
A;Reference number: S14707, MUID:90316097, PMID:2164470
A;Molecule type: mRNA
A;Accession: S14708
A;Residues: 1-420 <MOO>
A;Cross-references: UNIPROT:P18266; UNIPARC:UPI000012DDC0; EMBL:X53428; NID:G56333; PIDN:
A;Note: the author translated the codon ATG for residue 240 as Val
R;Ishiguro, K.; Shiratsuchi, A.; Sato, S.; Omori, A.; Arioka, M.; Kobayashi, S.; Uchida,
FEBS Lett. 325, 167-172, 1993
A;Title: Glycogen synthase kinase 3-beta is identical to tau protein kinase I generating
A;Reference number: S33741; MUID:93307488; PMID:7696508
A;Accession: S33741
A;Molecule type: mRNA
A;Residues: 1-239, 'V', 241-420 <ISH>
A;Cross-references: UNIPARC:UPI00000018B4; EMBL:X73653; NID:G402651; PIDN:CAA52020.1; PIDN:
A;Accession: S36729
A;Molecule type: protein
A;Residues: 37-58; 61-74; 151-158; 293-316; 318-325; 327-332; 351-368; 370-375 <ISH2>
A;Cross-references: UNIPARC:UPI0000172536; UNIPARC:UPI0000172537; UNIPARC:UPI0000172538;
S3D
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;54-315/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;85/Active site: Lys #status predicted
Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.2e-88;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 11 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VIGNSGFVVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VIGNSGFVVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIVRLRYFFYSYG 120
QY 131 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLPFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLPFRSLAYIHSFGICHR 180
QY 191 DIKPQNLLDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIFPGDSGVDQVLEIIVKVLGTPREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPGDSGVDQVLEIIVKVLGTPREQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPTTPEALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
Db 361 NFFTQELSSNPPLATILIPPHARI 384

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Db 361 NFFTQELSSNPPLATILIPPHARI 384

RESULT 3
I51425
intracellular kinase (EC 2.7.1.1-) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51425
R;Pierce, S.B.; Kimelman, D.
Development 121, 755-765, 1995
A;Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A;Reference number: I51425; MUID:95237008; PMID:7720590
A;Accession: I51425
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-420 <PIE>
A;Cross-references: UNIPROT:Q91757; UNIPARC:UPI00000FB682; GB:L38492; NID:G727189; PIDN:
C;Genetics:
C;Gene: Xgsk-3
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;54-315/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;85/Active site: Lys #status predicted
Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 6.5e-85;
Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 11 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFGSMKVS RDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VIGNSGFVVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIVRLRYFFYSYG 130
Db 61 VIGNSGFVVYQAKLDCSGELVAIKKVLQDKRPNKRELQIMRKLDHCNIVRLRYFFYSYG 120
QY 131 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLPFRSLAYIHSFGICHR 190
Db 121 EKDEVYLNVLVDYVPETVYRVARHYSRAKQTLPIVYVKLYMQLPFRSLAYIHSFGICHR 180
QY 191 DIKPQNLLDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
Db 181 DIKPQNLLDPDPAVLKCLDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240
QY 251 WSAGCVLAELLGQPIFPGDSGVDQVLEIIVKVLGTPREQIREMNPNTYEFKFPQIKAH 310
Db 241 WSAGCVLAELLGQPIFPGDSGVDQVLEIIVKVLGTPREQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPTTPEALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTTPEALCSRLLEYTPPTARLTPLCAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 393
Db 361 NFFTQELSSNPPLATILIPPHARI 383

RESULT 4
I51692
glycogen synthase kinase (EC 2.7.1.1-) 3 beta - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51692
R;Dominguez, I.; Itoh, K.; Sokol, S.Y.
Proc. Natl. Acad. Sci. U.S.A. 92, 8498-8502, 1995
A;Title: Role of glycogen synthase kinase 3 beta as a negative regulator of dorsoventral
A;Reference number: I51692; MUID:95396823; PMID:7667318
A;Accession: I51692
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-420 <DOM>

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A;Cross-references: UNIPROT:Q91627; UNIPARC:UPI000000FBE97; EMBL:U31862; NID:gl000734; Pf C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;54-315/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
F;85/Active site: Lys #status predicted

Query Match 92.4%; Score 1923; DB 2; Length 420;
Best Local Similarity 95.0%; Pred. No. 1.6e-84;
Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

```
QY 11 MSGRPRTTSFAESCKPVQPSAFSGSMKVS RDKGSKVTTVATPGQGPDRPQSVSYDTTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGSMKVS RDKGSKVTTVATPGQGPDRPQSVSYDTTK 60

QY 71 VINGSGFVVYQAKLDCSGELVAIKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKVLQDKRFKNRELQIMRKLDHCNIVRLRYFFYSYG 120

QY 131 EKDEVYLVNLDVVPETVTVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDEVYLVNLDVVPETVTVARHYSRAKQALPIIYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPQNLLDPDPTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
DB 181 DIKPQNLLDPDPTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYTSIDV 240

QY 251 WSAGCVLAELLGQPIFPFGSDGVDOLVEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 310
DB 241 WSAGCVLAELLGQPIFPFGSDGVDOLVEIKVLGTPTREQIREMNPNTYEFKPKQIAHP 300

QY 311 WTKVFRPRTPEAIALCSRLLEYTPPTARLTPLCAHSAFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEAIALCSRLLEYTPPTARLTPLCAHSAFDELDPNVKHPNGRDTPALF 360

QY 371 NPTQELSSNPPLATILIPPHAR 393
DB 361 NPTQELSSNPPLATILIPPHAR 383
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RESULT 5

TVTKA

protein kinase (EC 2.7.1.37) GSK-3-alpha - rat
N;Alternate names: factor A; glycogen synthase kinase 3 alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S14707
R;Woodgett, J.R.
EMBO J. 9, 2431-2438, 1990
A;Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
A;Reference number: S14707; MUID:90316097; PMID:2164470
A;Accession: S14707
A;Molecule type: mRNA
A;Residues: 1-483 <WO>
A;Cross-references: UNIPROT:PI8265; UNIPARC:UPI000012DDBF; EMBL:X53427; NID:956331; PIDN C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k F;117-378/Domain: protein kinase homology <KIN>
F;125-133/Region: protein kinase ATP-binding motif
F;148/Active site: Lys #status predicted

Query Match 77.2%; Score 1607; DB 1; Length 483;
Best Local Similarity 80.6%; Pred. No. 1.6e-69;
Matches 312; Conservative 23; Mismatches 38; Indels 14; Gaps 3;

```
QY 8 GGMGSGRPRT-TSPAESCKPVQPSAFSGSMKVS RDKGSKVTTVATPGQGPDRPQSVSY 66
DB 73 GGGSGGGFGAGTSPFP-----GVKLR--DSGKVTTVATLGQGPERSQEVAY 119

QY 67 TDTKVIKNGSGFVVYQAKLDCSGELVAIKVLQDKRFKNRELQIMRKLDHCNIVRLRYFF 126
DB 120 TDTKVIKNGSGFVVYQAKLAEATRELVAIKVLQDKRFKNRELQIMRKLDHCNIVRLRYFF 179
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QY 127 YSSGEKKDEVYLVNLDVVPETVTVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSFG 186
DB 180 YSSGEKKDEVYLVNLDVVPETVTVARHYSRAKQTLPIVIVKLYMYQLFRSLAYIHSQ 239

QY 187 ICHRDIKPQNLLDPDPTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYS 246
DB 240 VCHRDIKPQNLLDPDPTAVLKLDFGSAKOLVRGEPNVSYICSRYYRAPELIFGATDYS 299

QY 247 SIDWSAGCVLAELLGQPIFPFGSDGVDOLVEIKVLGTPTREQIREMNPNTYEFKPKQI 306
DB 300 SIDWSAGCVLAELLGQPIFPFGSDGVDOLVEIKVLGTPTREQIREMNPNTYEFKPKQI 359

QY 307 KAHPTWKVFRPRTPEAIALCSRLLEYTPPTARLTPLCAHSAFDELDPNVKHPNGRDT 366
DB 360 KAHPTWKVFRPRTPEAIALCSRLLEYTPPTARLTPLCAHSAFDELDPNVKHPNGRDT 419

QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
DB 420 PPLFNFPSPGELSLOPSLNAILIPHLR 446
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RESULT 6

S35327

protein kinase sg39 (EC 2.7.1.1-) (clone pNB39) - fruit fly (Drosophila melanogaster)
N;Alternate names: zw3-A
C;Contains: protein kinase (EC 2.7.1.37)
C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
C;Accession: S35327; S35326; S35329; A4431; S11675; S10931; S35421; S35422; S35424
R;Ruel, L.; Pantescio, V.; Lutz, Y.; Simpson, P.; Bourouis, M.
EMBO J. 12, 1657-1669, 1993

A;Title: Functional significance of a family of protein kinases encoded at the shaggy loc A;Reference number: S35325; MUID:93223707; PMID:8467811
A;Accession: S35327

A;Molecule type: mRNA

A;Residues: 1-575 <RUE>

A;Cross-references: UNIPROT:PI8431; UNIPARC:UPI000002B384; EMBL:X70863; NID:g11145; PIDN A;Accession: S35326

A;Molecule type: mRNA

A;Residues: 1-196, 'R', 198-394, 'D', 396-512, 'D', 514 <RU2>

A;Cross-references: UNIPARC:UPI000016BD6A; EMBL:X70862; NID:g11143; PIDN:CAA50212.1; PID A;Accession: S35329

A;Molecule type: mRNA

A;Residues: 1-42 <RU3>

A;Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CAA50215.1; PID A;Note: the translation of the nucleotide sequence is not complete in this paper

R;Siegfried, E.; Chou, T.B.; Perrimon, N.

Cell 71, 1167-1179, 1992

A;Title: wingless signaling acts through zeste-white 3, the Drosophila homolog of glycog A;Reference number: A44331; MUID:93113685; PMID:1335365

A;Accession: A44331

A;Molecule type: mRNA

A;Residues: 1-445, 'R', 447-510, 'DVTDS', <SIE>

A;Cross-references: UNIPARC:UPI000017A460

R;Bourouis, M.; Moore, P.; Ruel, L.; Grau, Y.; Heitzler, P.; Simpson, P.

EMBO J. 9, 2877-2884, 1990

A;Title: An early embryonic product of the gene shaggy encodes a serine/threonine protei A;Reference number: S11675; MUID:90361000; PMID:2118107

A;Accession: S11675

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-243, 'I', 245-405, 'A', 407-512, 'D', 514 <BOU>

A;Cross-references: UNIPARC:UPI000016BD69; EMBL:X53332; NID:g10895; PIDN:CAA37419.1; PID R;Siegfried, E.; Perkins, L.A.; Capaci, T.M.; Perrimon, N.

Nature 345, 825-829, 1990

A;Title: Putative protein kinase product of the Drosophila segment-polarity gene zeste-w A;Reference number: S10931; MUID:90294930; PMID:2113617

A;Accession: S10931

A;Molecule type: mRNA

A;Residues: 1-289 <ST2>

A;Cross-references: UNIPARC:UPI000016BE19; EMBL:X54005; NID:c8859; PIDN:CAA37951.1; PID: A;Experimental source: ovarian cdna library

C;Genetics:
A;Gene: FlyBase:egg
A;Cross-references: FlyBase:FBgn0003371
C;Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threonine kinase
F;52-313/Domain: protein kinase homology <KIN>
F;60-68/Region: protein kinase ATP-binding motif

Query Match 76.4%; Score 1590.5; DB 2; Length 575;
Best Local Similarity 79.6%; Pred. No. 1.1e-68;
Matches 305; Conservative 32; Mismatches 41; Indels 5; Gaps 4;

QY 11 MSGRPRTTSPAECKPVQPS-AFGSMKVSRRDGGSKVTTVVATPGQDPDRQSVSTDT 69
DB 1 MSGRPRTSSPAENK--QSPSLVGGVTC-SRDGSKITTVVATPGQDTRQVQSVSTDT 57

QY 70 KVIKNGSGFVYVQAKLDCDSELVAIKKVLQDKRFKRELQIMRKLHCHNCNIRLRYFFYS 129
DB 58 KVIKNGSGFVYVQAKLDCDSELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRLRYFFYS 117

QY 130 GEKKDEVILNLVDYVPETVYRVARHYSRAKOTLPVYVYKLYMYQLFRSLAYTHSGICH 189
DB 118 GEKKDEVILNLVLEYPETVYRVARQYAKTKQTIPINFIRLYMYQLFRSLAYTHSGICH 177

QY 190 RDIKPQNLDDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYSID 249
DB 178 RDIKPQNLDDPTAVLKLCDFGSAKQLLHGEPNVSYICSRYYRAPELIFGAINYTKID 237

QY 250 VWSAGCVLAELLGQPIFPDGSQDQVLEIKVLGTPTRREQIREMNPNTPEKPPQIKAH 309
DB 238 VWSAGCVLAELLGQPIFPDGSQDQVLEIKVLGTPTRREQIREMNPNTPEKPPQIKSH 297

QY 310 PWTQVFRPPTPEAIALCSRLLEYTPARTLPLEACAHSPFDELRLDPNVKHPNGRDTPA 368
DB 298 PWTQVFRPRTPEAINLVSLLEYTPSARITPLKACAHPPFDELRLMEGHNHTLPNGRDMPP 357

QY 369 LFNFTTQELSSNPPLATILIPPH 391
DB 358 LFNFTTEHLSIQPSLVPLQPKH 380

RESULT 7
S10932
probable protein kinase zeste-white3 (EC 2.7.1.1-) (clone cK25) - fruit-fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
C;Accession: S10932
R;Siegfried, B.; Perkins, L.A.; Capaci, T.M.; Perrimon, N.
Nature 345, 825-829, 1990
A;Title: Putative protein kinase product of the Drosophila segment-polarity gene zeste-white3
A;Reference number: S10931; MUID: 90294930; PMID: 2113617
A;Accession: S10932
A;Molecule type: mRNA
A;Residues: 1-733 <SITE>
A;Cross-references: UNIPARC:UPI000016BE18; EMBL:X54006; NID:98857; PIDN:CAA37952.1; PID: S10932
A;Experimental source: embryonic CDNA library
A;Note: it is uncertain whether Met-1 or Met-44 is the initiator or whether translation starts at Met-1
C;Genetics:
A;Gene: zw3
A;Cross-references: FlyBase:FBgn0003371
C;Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threonine kinase
F;285-546/Domain: protein kinase homology <KIN>
F;293-301/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1542.5; DB 2; Length 733;
Best Local Similarity 75.9%; Pred. No. 2.5e-66;
Matches 296; Conservative 36; Mismatches 47; Indels 11; Gaps 3;

QY 7 EGGGMSGRPRTTSPAECKPVQPS-AFGSMKVSRRDGGSKVTTVVATPGQDPDRQ 62
DB 230 DGGGENVKTAKLARTQSCVSWTKVQK-----FKNLTGRDGSKITTVVATPGQDTRVQ 283

QY 63 EVSYTDTKVIKNGSGFVYVQAKLDCDSELVAIKKVLQDKRFKRELQIMRKLHCHNCNIRL 122
DB 61 EVSYTDTKVIKNGSGFVYVQAKLDCDSELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRL 122

DB 284 EYSYTTDKVIKNGSGFVYVQAKLDCDSELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRL 343
QY 123 RYFFYSSGKKDDEVILNLVDYVPETVYRVARHYSRAKOTLPVYVYKLYMYQLFRSLAYI 182
DB 344 LYFFYSSGKKDDEVILNLVLEYPETVYRVARQYAKTKQTIPINFIRLYMYQLFRSLAYI 403

QY 183 HSPGICHRODKPQNLDDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGAT 242
DB 404 HSLGICHRODKPQNLDDPTAVLKLCDFGSAKQLLHGEPNVSYICSRYYRAPELIFGAI 463

QY 243 DYTSSIDVMSAGCVLAELLGQPIFPDGSQDQVLEIKVLGTPTRREQIREMNPNTPEK 302
DB 464 NYTKIDVMSAGCVLAELLGQPIFPDGSQDQVLEIKVLGTPTRREQIREMNPNTPEK 523

QY 303 FPOIKAHPTKVPRTPEAIALCSRLLEYTPARTLPLEACAHSPFDELRLDPNVKHP 361
DB 524 FPOIKSHPTKVPRTPEAIALCSRLLEYTPSARITPLKACAHPPFDELRLMEGHNHTLP 583

QY 362 NGRDTEALFNFTTQELSSNPPLATILIPPH 391
DB 584 NGRDMPLEFNFTTEHLSIQPSLVPLQPKH 613

RESULT 8
S35423
protein kinase egg46 (EC 2.7.1.1-) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C;Accession: S35423
R;Ruel, L.; Pantescio, V.; Lutz, Y.; Simpson, P.; Bourouis, M.
EMBO J 12, 1657-1669, 1993
A;Title: Functional significance of a family of protein kinases encoded at the shaggy locus
A;Reference number: S35325; MUID: 93223707; PMID: 8467811
A;Accession: S35328
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1067 <SUB>
A;Cross-references: UNIPARC:UPI000013591B; EMBL:X70864; NID:911147; PIDN:CAA50214.1; PID: S35423
C;Genetics:
A;Gene: FlyBase:egg
A;Cross-references: FlyBase:FBgn0003371
C;Keywords: ATP; phosphotransferase
F;605-866/Domain: protein kinase homology <KIN>
F;613-621/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1542.5; DB 2; Length 1067;
Best Local Similarity 75.9%; Pred. No. 3.5e-66;
Matches 296; Conservative 36; Mismatches 47; Indels 11; Gaps 3;

QY 7 EGGGMSGRPRTTSPAECKPVQPS-AFGSMKVSRRDGGSKVTTVVATPGQDPDRQ 62
DB 550 DGGGENVKTAKLARTQSCVSWTKVQK-----FKNLTGRDGSKITTVVATPGQDTRVQ 603

QY 63 EVSYTDTKVIKNGSGFVYVQAKLDCDSELVAIKKVLQDKRFKRELQIMRKLHCHNCNIRL 122
DB 604 EYSYTTDKVIKNGSGFVYVQAKLDCDSELVAIKKVLQDRRFKRELQIMRKLHCHNCNIRL 663

QY 123 RYFFYSSGKKDDEVILNLVDYVPETVYRVARHYSRAKOTLPVYVYKLYMYQLFRSLAYI 182
DB 664 LYFFYSSGKKDDEVILNLVLEYPETVYRVARQYAKTKQTIPINFIRLYMYQLFRSLAYI 723

QY 183 HSPGICHRODKPQNLDDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGAT 242
DB 724 HSLGICHRODKPQNLDDPTAVLKLCDFGSAKQLLHGEPNVSYICSRYYRAPELIFGAI 783

QY 243 DYTSSIDVMSAGCVLAELLGQPIFPDGSQDQVLEIKVLGTPTRREQIREMNPNTPEK 302
DB 784 NYTKIDVMSAGCVLAELLGQPIFPDGSQDQVLEIKVLGTPTRREQIREMNPNTPEK 843

QY 303 FPOIKAHPTKVPRTPEAIALCSRLLEYTPARTLPLEACAHSPFDELRLDPNVKHP 361
DB 844 FPOIKSHPTKVPRTPEAIALCSRLLEYTPSARITPLKACAHPPFDELRLMEGHNHTLP 903

A;Residues: 1-472 <GI>
A;Cross-references: UNIPROT:Q96287; UNIPARC:UPI0000000E6A; EMBL:AF058919; NID:g3047100;
C;Genetics:
A;Gene: ATSP:F6N23.11
A;Map position: 5
A;Introns: 21/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 353/3; 385/3; 413/3; 4
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; protein kinase
F;136-397/Domain: protein kinase homology <KIN>
F;144-152/Region: protein kinase ATP-binding motif
F;167/Active site: Lys #status predicted

Query Match 60.5%; Score 1256; DB 1; Length 472;
Best Local Similarity 61.2%; Pred. No. 5e-53;
Matches 250; Conservative 54; Mismatches 74; Indels 28; Gaps 9;

QY 10 GMSGRPRTTTSAESCKPV--QPSAFGSMKV-----SRDKD-----GSKVTVV 51
DB 67 GTSNVP-----AVSEKPVDDQLPDVMIEMKIRDERNANREDKMETTVVNGSGTGTQVI 121

QY 52 ATPGQGPDRP-QEVSYTDTKVINGSGFVVYQAKLDCSGELVAIKKVLQDKRPFKNRELQ 109
DB 122 TTVVGRDGRPKQTISTYMAERVVGSGFVVYQAKCLETGETVAIKKVLQDKRYKNRELQ 181

QY 110 IMKLDHCNIVRLRYFFYSSEKDEVLNLVDYVPETVYVARHYSRAKQTLPIVYVK 169
DB 182 IMRLQHPNVVRLRHSPFTTD-KDELYLNLVLEYPETVYVARHYSRAKQTLPIVYVK 240

QY 170 LYMQLFRSLAYTH-SFGICHRDIKPNQLLDPTAVLKLCDFGSAKOLVRGEPNVSYIC 228
DB 241 LYTQICRALAYIHNSIGVCHRDIKPNQLLVNPHTHQKICDFGSAKOLVRGEPNVSYIC 300

QY 229 SRYRAPELIFGATDYTSSIDVMSAGCVLAELLIGQPIFPDGSQVDQLEIIVKLGTPTR 288
DB 301 SRYRAPELIFGATEYTNADMSSGCVMAELLIGQPIFPDGSQVDQLEIIVKLGTPTR 360

QY 289 EQIREMNPNTYEFKFPQIKAHPTKVFPRTPPEAIALCSRLLLEYTPTARLTPLCAHNS 348
DB 361 EEIRCMNPNTYEFKFPQIKAHPTKVFPRTPPEAIALCSRLLLEYTPTARLTPLCAHNS 420

QY 349 FDELDPNVKHPNGRDTPALFNFTTOELSSNP-PLATILIPPHAR 393
DB 421 FFDDLDPNVSLNPGRLPPLFNFTTOELSSNP-PLATILIPPHAR 466

RESULT 15
S37642
protein kinase MSK-3 (EC 2.7.1.-) [similarity] - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: S37642
R;Pay, A.; Jonak, C.; Boegre, L.; Meskiane, I.; Mairinger, T.; Szalay, A.; Heberle-Bors,
plant J. 3, 847-856, 1993
A;Title: The MSK family of alfalfa protein kinase genes encodes homologues of shaggy/gly
A;Reference number: S37642; MUID:94004996; PMID:8401615
A;Accession: S37642
A;Molecule type: mRNA
A;Residues: 1-412 <PAY>
A;Cross-references: UNIPARC:UPI000016D9F3; EMBL:X68409; NID:g311147; PIDN:CAA48472.1; PI
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;73-334/Domain: protein kinase homology <KIN>
F;81-89/Region: protein kinase ATP-binding motif
F;104/Active site: Lys #status predicted

Query Match 60.4%; Score 1256; DB 1; Length 412;
Best Local Similarity 61.2%; Pred. No. 5e-53;
Matches 248; Conservative 55; Mismatches 82; Indels 20; Gaps 8;

QY 6 MEGGSGMGRPRTTTSAESCKPV--QPSAFGSMKVSRDK-----DGSKVTT---VV 51
DB 2 MASGGVA--PASGFIDKNASSGVGEKLPPEWMDKIRDDKEMEAATVVDGNGTGTGHIV 59

Search completed: September 15, 2006, 17:12:54
Job time : 42 secs

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